

GenCore version 5.1.1.6
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DN nucleic - nucleic search, using sw model

Run on: January 31, 2004, 00:52:19 ; Search time 114 Seconds
(without alignments)
7035.028 Million cell updates/sec

Title: US-09-890-456-8

Perfect score: 1817

Sequence: 1 ggacataaaagggaaca.....aagttgcataaccatcaaaa 1817

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*

5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	196.4	10.8	2315	4	US-09-152-060-48
C 2	194.2	10.7	3856	4	US-09-620-312D-451
C 3	88.8	4.9	1732	4	US-09-152-060-30
C 4	49.6	2.7	4453	4	US-09-146-053-5
C 5	48	2.6	6804	4	US-09-740-041-3
C 6	47.6	2.6	703	3	US-09-313-300-6
C 7	44.8	2.5	5824	4	US-09-620-312D-72
C 8	44.4	2.4	50000	4	US-09-146-053-3
C 9	42.4	2.3	81001	4	US-09-750-580-1
C 10	42	2.3	2697	4	US-09-620-312D-401
C 11	41.6	2.3	62804	4	US-09-800-960-3
C 12	41	2.3	10627	1	US-08-060-925A-12
C 13	41	2.3	51719	4	US-09-918-686-2
C 14	41	2.3	92139	4	US-09-918-686-1
C 15	40.8	2.2	18853	4	US-09-820-005-3
C 16	40.8	2.2	51719	4	US-09-918-686-2
C 17	40.8	2.2	92139	4	US-09-918-686-1
C 18	40.6	2.2	6953	1	US-07-805-123C-2
C 19	40.6	2.2	6953	1	US-08-033-081B-2
C 20	40.6	2.2	7301	4	US-09-816-094-3
C 21	40.6	2.2	36741	3	US-09-301-665-3
C 22	40.6	2.2	50000	4	US-09-146-053-3
C 23	40.6	2.2	55298	4	US-09-491-356C-1
C 24	40.4	2.2	1601	4	US-09-220-132-182
C 25	39.6	2.2	4453	4	US-09-146-053-5
C 26	39.2	2.2	377	3	US-09-328-111-672
C 27	39.2	2.2	1454	1	US-08-467-155A-2

C 28	39.2	2.2	1454	2	US-08-628-198-2	Sequence 2, Appli
C 29	39.2	2.2	1454	3	US-09-201-038-2	Sequence 2, Appli
C 30	39.2	2.2	1454	5	PCT-US96-07343-2	Sequence 2, Appli
C 31	39.2	2.2	7218	1	US-08-232-463-14	Sequence 14, Appli
C 32	39.2	2.2	24707	4	US-09-740-027-3	Sequence 3, Appli
C 33	39	2.1	3795	1	US-08-343-760A-1	Sequence 1, Appli
C 34	39	2.1	10014	3	US-08-927-219-130	Sequence 130, App
C 35	38.8	2.1	441	4	US-09-288-143-59	Sequence 59, Appli
C 36	38.8	2.1	11725	2	US-08-756-506-1	Sequence 1, Appli
C 37	38.6	2.1	4129	2	US-08-370-319C-12	Sequence 12, Appli
C 38	38.6	2.1	4129	3	US-09-224-834-12	Sequence 12, Appli
C 39	38.6	2.1	50000	4	US-09-146-053-4	Sequence 4, Appli
C 40	38.6	2.1	11282	4	US-09-754-250-3	Sequence 3, Appli
C 41	38.4	2.1	16063	4	US-09-801-052-3	Sequence 3, Appli
C 42	38.2	2.1	17138	3	US-09-813-819-3	Sequence 3, Appli
C 43	38.2	2.1	17138	4	US-09-920-048-3	Sequence 3, Appli
C 44	38.2	2.1	4403765	3	US-09-103-840A-2	Sequence 2, Appli
C 45	38.2	2.1	4411529	3	US-09-103-840A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-152-060-48/c
; Sequence 48, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 2315
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2264)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2312)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2315)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-152-060-48

Query Match		10.8%;	Score 196.4;	DB 4;	Length 2315;
Best Local Similarity		53.0%;	Pred. No. 4.8e-48;		
Matches		475;	Conservative	0;	Mismatches 406; Indels 15; Gaps 2;
2y	475	CAGACATGTTCTGCTTTTCCATGGAGAGATACCTCCCGCGAGAGCTGACCCCT	534		
Db	2063	CAGAGACATATTCGATGTTTCAAGACAGAGTACAGAGTGGTGAGAGTGCATCTT	2004		
2y	535	ACTTGGAGCCACAGGCTGATGTACTGCTCGCTGTACCTGCTCAGAGGGGCCCATG	594		
Db	2003	ACTTGGARCTTATGGTGGTTTACTGCTGGAATGCTGCTCAGAGAATGGGAATG	1944		
2y	595	TGAGTTGTTACGGCTCCACTGTCGGCTGTCCACTGTCGCCCGAGCTGTGACGGAGCCAC	654		
Db	1943	TGCTTTGAGCGGAGTCAGATGCCAAATGTTTCAATGGCTTTCTCTGTGCATATTCCTC	1884		
2y	655	AGCAATGCTGCTCCCAAGTGTGGACCTCACACTCCCTCTGACTC---CGSGCCCCAC	711		
Db	1883	ATCTGTGCTGCCCTCGCTGCCAGAGATCTCTTACCCCGAGTGAACAATAAGGTGACCA	1824		
Qy	712	CAAGTCTGTCAGACAGAGGACCATGTACCACACAGGAGAGATCTTCAGTGCCCATG	771		
Db	1823	GCAAGTCTTGGAGTACATATGGACAACTTACCAACATGAGAGCTGTTGTAGCTGAAG	1764		
Qy	772	AGCTGTTCCTCCCGCTGCCCAACACAGTGTCTCTGTGACCTGCACAGAGGGCCAGA	831		
Db	1763	GGCTCTTTCAGATCGGCAACCAANTCAATGCACCCAGTGCAGCTGTTCGGAGGGAACG	1704		
Qy	832	TCTACTGGGGCTCAAACTGCGCCCGAACAGGCTGCCAGACCCCTCCCGTGCAG	891		
Db	1703	TGATTTGGTCTCAAGACTTGCCCAAAATTAACCTGTGCTTCCCAAGTCTCTGTCCAG	1644		
Qy	892	ACTCTGCTGCCAAGCTGCAAGATGAGCAAGTGGCAATCGGATGAAGAGACAGTG	951		
Db	1643	ATTCTGCTGCCGGGTATGACAGAGAGTGGAACTGTTCATGGGAACATTTCTGATGGTG	1584		
Qy	952	TGCACTGCTCCA-----TGGGGTGAGACATCTCCAGATCCATGTTCCAGTG	999		
Db	1583	ATATCTTCGGCAACTGCCAACAGAGAACAGACATTTTACCACGGCTCTCACTATG	1524		
Qy	1000	ATGCTGGGAGAAAGAGAGGCGCGGACACCCCGCCCTCAGCGCTCAGCGCCCTCTGA	1059		
Db	1523	ATCTTCCCAAGCCGACAGGCTGGAGTGTGTCCCGCTTCTGGGGCCAGAAAGTCAAC	1464		
Qy	1060	GCTTCATCCTCGCCATTCAGACCCAGGAGGAGGAGGAGCAACATGTCAAGATCGTCC	1119		
Db	1463	GGGGAGCTCTTATGGATTCCCAAGCATCAGGAACCATTTGTGCAAAATTTGTCATATA	1404		
Qy	1120	TGAAGAGAAACATAAGAACCTGTGTGATGCGGGAGAGACGTACTCCACCGGGAGG	1179		
Db	1403	ACAAACACAGCATGACAAAGTGTGTGTTTCCAAATGGAAGACCTATTCTCATGGCGAGT	1344		
Qy	1180	TGTGGCACCGGCTTCCGCTGCTTCCGCGCTTCCGCTGCTATGCACTGTGAGG	1239		
Db	1343	CTTGGACCCCAACCTCCGGGCATTTGGCATTTGGAGTGTGTGTAATGTAATG	1284		
Qy	1240	ATGGCGCCAGGAGTCCAGCGTGTGACCTGTGCCACCGAGTACCCCTGCGCTACCCCG	1299		
Db	1283	TCACCAAGCAAGAGTGTGAAGAAATCCACTGCCCCCATCGATACCCCTGCAAGTATCCTC	1224		
Qy	1300	AGAAAGTGGTGGAGTGTGCAAGATTTGCCAGAGGACAAAGACACCCCTGGC	1355		
Db	1223	AAAAAATAGCGGAAATGTGCAAGGTGTGTCCAGAGAACTTCCAGGCCCAAGC	1168		

RESULT 2
US-09-620-312D-451
; Sequence 451, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod

APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yunging
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John, Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pc_fl_genes Version 1.0
SEQ ID NO 451
LENGTH: 3856
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (105)..(1481)
US-09-620-312D-451

Query Match		10.7%;	Score 194.2;	DB 4;	Length 3856;
Best Local Similarity		53.0%;	Pred. No. 2.9e-47;		
Matches		471;	Conservative	0;	Mismatches 403; Indels 15; Gaps 2;
Qy	475	CAGACATGTTCTGCTTTTCCATGGGAAGAGATACCTCCCGCGAGAGCTGGCACCCCT	534		
Db	202	CAGACATATTTGATGTTTCAAGACAGAAAGTACAGAGTGGTGAGAGATGGCATCTT	261		
Qy	535	ACTTGGAGCCACAGGCTGATGTACTGCTGGCTGTACTGCTGACAGGGCGCCCATG	594		
Db	262	ACCTGGAACCTTATGGTGTGTTTACTGCTGAATCTGCTGCTACAGAAATGGGAATG	321		
Qy	595	TGAGTTGTTACGGCTTCCACTGTCGGCTGTCCACTGCGCCCGCCCGCTGTGAGCGGAC	654		
Db	322	TGCTTTCAGCGGAGTCAGATGTCCAAATGTTCAATGCTTCTCTGTGCAATATCTCTC	381		
Qy	655	AGCAATGCTGCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTC---CGGGCCCCAC	711		
Db	382	ATCTGTGCTGCCCTCGCTGCCAGAGACTCTTTACCCCGAGTGAACAATAAGGTGACCA	441		
Qy	712	CAAAAGTCTGCCAGCACACGGGACCATGTACCAACACGGAGAGATTTTCAGTGCCCATG	771		
Db	442	GCAGTCTTGGAGTACATATGGGACAACTTACCAACATGGAGAGCTGTTCTGTAGCTGAAG	501		
Qy	772	AGCTGTTTCCCTCCCGCTGCCCAACCAAGTGTGTCCTCTGCAAGTGTGCAAGAGGSCCAGA	831		
Db	502	GGCTCTTTTCAAGATCGGCAACCAATCAATGCAACCCAGTCAGCTGTTTCGGAGGGAACG	561		
Qy	832	TCTACTGCGGCTCACAACTGCGCCCGCAACAGGCTGCCAGCACCCTCCCGCTGCCAG	891		
Db	562	TGTATTGTGCTCTCAAGACTTGGCCCCAAATTAACCTGTGCTTCCAGTCTCTGTCTCCAG	621		
Qy	892	ACTCTGCTGCCAAGCTGCAAGATGAGGCAAGTGAAGCAATCGGATGAAGAGGACAGTG	951		
Db	622	ATTCTTCTGCTCCCGGTATGAGAGGAGATGGAGACTGTGATGGGAACATTTCTGATGGTG	681		
Qy	952	TGCAGTGGCTCCA-----TGGGGTGAGACATCTCTCAGATTCATGTTTCCAGTG	999		
Db	682	ATATCTTCCGGCAACCTGCCCAACAGAGAAAGCAAGACATTTTACCACCGCTCTCACTATG	741		

1000 ATGCTGGGAAAGAGAGCCCGGACACCCAGCCCTGAGCCCTGAGCCCTCTGA 1059
b 742 ATCTTCCCAAGCCGACAGGCTGGAGGTGTGCTGCTTTCTTGGGCGCAGAAATCACC 801
1060 GCTTCATCCCTCGCCACTTCAGACCCCAAGGAGCAGCAGCAGCAACTGTCAAGATCGTCC 1119
b 802 GGGGAGCTTTATGATTTCCACAGCAGCATCAGGAACATTGTGCAAAATTGTCAATA 861
1120 TGAAGGAGAAACATAAGAACCTGTGTGATGCGCGGAAAGACGTACTCCACCGGGAGG 1179
b 862 ACAACACAGCATGACAAAGTGTGTGTTTCCATGGAAGACCTATTCTCATGGCGAGT 921
1180 TGTGACACCGGCTTCGCTGCTTGGCCCTTGGCCCTGCTGATGCACTGACCTGTGAGG 1239
b 922 CTGGCACCACCAACCTCCGGGCAATTTGGCAATTTGGAGTGTGCTATGTACTTGTAAATG 981
1240 ATGGCGCCGAGACTGCCAGCTGTGACCTGTCCACCGAGTACCCCTGCGCTCACCCCG 1299
b 982 TCACCAAGCAAGAGTGTAAAGAAATCCACTGCCCAATCGATACCCCTGCAAGTATCCTC 1041
1300 AGAAAGTGTGCTGGAAGTGTGCAAGATTGCGCAGAGGACAAAGCAGA 1348
b 1042 AAAAAATAGACGGAAATGCTGCAAGTGTGTCAGGTAAAAAACA 1090

RESULT 3
3-09-152-060-30
Sequence 30, Application US/09152060
Patent No. 6448230
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P1 US
CURRENT APPLICATION NUMBER: US/09/152,060
EARLIER FILING DATE: 1998-09-11
EARLIER APPLICATION NUMBER: PCT/US98/04858
EARLIER FILING DATE: 1998-03-12
EARLIER APPLICATION NUMBER: 60/040,762
EARLIER FILING DATE: 1997-03-14
EARLIER APPLICATION NUMBER: 60/040,710
EARLIER FILING DATE: 1997-03-14
EARLIER APPLICATION NUMBER: 60/050,934
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,100
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,357
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,189
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/057,765
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/068,368
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 30
LENGTH: 1732
TYPE: DNA
ORGANISM: Homo sapiens

3-09-152-060-30
Query Match 4.9%; Score 88.8; DB 4; Length 1732;
Best Local Similarity 48.9%; Pred. No. 3.6e-16;
Matches 268; Conservative 3; Mismatches 265; Indels 12; Gaps 1;

820 CAGAGGCGCAGATCTACTCGGCTTACACACCTGCCCCGACAGGCTGCCAGCACC 879
4 CGAGGGAACCTGTATTGTGCTCTCAAGWMTTGGCCCAWATTAACTGTGCTTCCAG 63

880 TCCCGCTGCCAGACTCTCTGCTGCAAGCTTGCAAGATGAGGCAAGTGAGCAATCGGATG 939

Db 64 TCTCTTTCCAGATTCCTGCTGCGGGTATGACAGAGAGATGGAGAACTGTCTATGGAAAC 123
QY 940 AAGAGACAGTGTGAGTGTGCTCCAT-----GGGGTGAAGACATCTCTCAGGATC 987
Db 124 ATTCTGATGATATCTTCCGGCACTGCCAACAGAGAGCAAGACATTTCTTACCACC 183
QY 988 CATGTTCCAGTGTGAGTGGGAGAAAGAGAGCCCGGACACCCCGACCCCTGACCTGACCTCA 1047
Db 184 GCTCTCACTATGATCTCCACCAAGCGCAGAGGTGTGAGGTCTGTCCCGCTTTCTCGGG 243
QY 1048 GGGCCCTCTGAGCTTCATCCCTGCGCACTTACAGCCAGGAGCAGGACCAACTG 1107
Db 244 CCAGAGTCCACCGGGAGCTCTTATGATTTCCAGCAAGCATCAGGAACCATTTGTCRAA 303
QY 1108 TCAAGATCGTCTGAGAGGAAACATAAGAAAGCTGTGTGATGCTGCGGGAGAGCTACT 1167
Db 304 TTGTCTATCAATACAAACACAGCATGGAAGAATGTTTCCAAATGGAAGACCTATT 363
QY 1168 CCCAGGGGAGTGTGGCACCCCGCTTCCGTGCTTCCGGCCCTTGGCCCTGCACTCTAT 1227
Db 364 CTCATGGCAGTCTGCGCACCCCAACCTCCGGCATTTGGCATTTGGAGTGTGCTAT 423
QY 1228 GCACTGTGAGGATGCGCCAGGACTGCGAGGTGTGACTGTCCACCGAGTACCCT 1287
Db 424 GTACTGTAAATGTACCAAGCAAGAGTGTAAAGAAATCCACTGCCCAATCGATACCCCT 483
QY 1288 GCGGTACCCCGAGAAAGTGGCTGGGAAAGTGTGCAAGATTTGCCAGAGCAAGACG 1347
Db 484 GCAAGTATCTCAAAAAATAGACGGAATAATGCTGCAAGGTGTGTCAGAGGATGTC 543
QY 1348 ACCCTGGC 1355
Db 544 GCCAAGC 551

RESULT 4
US-09-146-053-5
Sequence 5, Application US/09146053A
Patent No. 6399349
GENERAL INFORMATION:
APPLICANT: Ryan, James W.
APPLICANT: Sprinkle, Terry Joe Curtis
APPLICANT: Venema, Richard C.
TITLE OF INVENTION: Human Aminopeptidase P Gene
FILE REFERENCE: MCG103
CURRENT APPLICATION NUMBER: US/09/146,053A
CURRENT FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/057,854
EARLIER FILING DATE: 1997-09-02
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 5
LENGTH: 44453
TYPE: DNA
ORGANISM: Homo sapiens

US-09-146-053-5
Query Match 2.7%; Score 49.6; DB 4; Length 44453;
Best Local Similarity 69.8%; Pred. No. 0.00097;
Matches 67; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 1508 AGATGAGGAACCTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAA 1567
Db 26816 AGATGAGGAAGCCGAGGACAGAGAGGTCAAGTAACTTGTGCTGAGGTGTCACACAGCCAGAA 26875

QY 1568 TCTTCCACTTGTAGTCAAGATCAAGAAAGTCAAGAAC 1603
Db 26876 AGTGGAGATCTGGGATTTGAACGAAGTCTGTGAGC 26911

RESULT 5
US-09-740-041-3

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Sequence 3, Application US/09740041
Patent No. 6562593
GENERAL INFORMATION:
APPLICANT: MERKULOV, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001001
CURRENT APPLICATION NUMBER: US/09/740,041
CURRENT FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 66804
TYPE: DNA
ORGANISM: Human
US-09-740-041-3

Query Match      2.6%; Score 48; DB 4; Length 66804;
Best Local Similarity 84.4%; Pred. No. 0.0036;
Matches 54; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Y 1504 TAAAGATGAGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCC 1563
DB 5244 TTACAGATGAGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCT 5303

Y 1564 AGAA 1567
DB 5304 ATAA 5307

RESULT 6
JS-09-313-300-6
Sequence 6, Application US/09313300
Patent No. 622027
GENERAL INFORMATION:
APPLICANT: Kaser, Matthew, R.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Tom, Y.
APPLICANT: Baughn, Mariah, R.
APPLICANT: Azimzai, Valda
TITLE OF INVENTION: MOLECULES EXPRESSED IN HIPPOCAMPUS
FILE REFERENCE: PB-0012 US
CURRENT APPLICATION NUMBER: US/09/313,300
CURRENT FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PERL Program
SEQ ID NO 6
LENGTH: 703
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY:
OTHER INFORMATION: 1941247
PUBLICATION INFORMATION:
US-09-313-300-6

Query Match      2.6%; Score 47.6; DB 3; Length 703;
Best Local Similarity 85.5%; Pred. No. 0.00037;
Matches 53; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Y 1504 TAAAGATGAGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCC 1563
DB 554 TTACAGATGGGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCG 613

Y 1564 AG 1565
DB 614 AG 615

RESULT 7
US-09-620-312D-72/c
```

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Sequence 72, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yunding
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Dmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 794CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 72
LENGTH: 5824
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (590)..(5824)
US-09-620-312D-72

Query Match      2.5%; Score 44.8; DB 4; Length 5824;
Best Local Similarity 81.2%; Pred. No. 0.0082;
Matches 52; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Y 1504 TAAAGATGAGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCC 1563
DB 139 TCATAGATGAGAACTGAGGCTCAGAGAGGTGAAGTATCTTGTCCCAAGATCACACAGCT 80

Y 1564 AGAA 1567
DB 79 AGTA 76

RESULT 8
US-09-146-053-3
Sequence 3, Application US/09146053A
Patent No. 6399349
GENERAL INFORMATION:
APPLICANT: Ryan, James W.
APPLICANT: Sprinkle, Terry Joe Curtis
APPLICANT: Venema, Richard C.
TITLE OF INVENTION: Human Aminopeptidase P Gene
FILE REFERENCE: MCG103
CURRENT APPLICATION NUMBER: US/09/146,053A
CURRENT FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/057,854
EARLIER FILING DATE: 1997-09-02
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 50000
TYPE: DNA
ORGANISM: Homo sapiens
```


US-09-146-053-3

Query Match 2.4%; Score 44.4; DB 4; Length 50000;
Best Local Similarity 82.3%; Pred. No. 0.036;
Matches 51; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1504 TAAAGATGAGGAACTGAGGCTCAGAGGTCAGTACCTGGCCCAAGGCCACACAGCC 1563

Db 18961 TTACGATGAGGACATTGAGGCTCAGAGAGGTCAACAGGTTGCTCAAGGCCACACAGCC 19020

Qy 1564 AG 1565

Db 19021 AG 19022

RESULT 9

US-09-750-580-1/c

; Sequence 1, Application US/09750580

; Patent No. 6455280

; GENERAL INFORMATION:

; APPLICANT: Yen, Frances

; APPLICANT: Denison, Blake

; APPLICANT: Bour, Barbara

; APPLICANT: Bihain, Bernard

; APPLICANT: Dumas Milne Edwards, Jean-Baptiste

; APPLICANT: Duclert, Aymeric

; APPLICANT: Bouguieret, Lydie

; APPLICANT: Ebbets-Reed, Dana

; APPLICANT: Salter-Cid, Luisa

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH

; FILE REFERENCE: 89 US2.CIP

; CURRENT APPLICATION NUMBER: US/09/750,580

; CURRENT FILING DATE: 2000-12-28

; PRIOR APPLICATION NUMBER: US 09/599,362

; PRIOR FILING DATE: 2000-06-21

; PRIOR APPLICATION NUMBER: PCT/IB99/02058

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: US 49/469/099

; PRIOR FILING DATE: 1999-12-21

; PRIOR APPLICATION NUMBER: US 60/113,686

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: US 60/141,032

; PRIOR FILING DATE: 1999-06-25

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: Patent.pm

; SEQ ID NO 1

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: 10945..12946

; OTHER INFORMATION: 5'regulatory region

; NAME/KEY: exon

; LOCATION: 12947..12958

; OTHER INFORMATION: exon 1

; NAME/KEY: exon

; LOCATION: 13470..13526

; OTHER INFORMATION: exon 2

; NAME/KEY: exon

; LOCATION: 13641..13752

; OTHER INFORMATION: exon 3

; NAME/KEY: exon

; LOCATION: 14271..15968

; OTHER INFORMATION: exon 4

; NAME/KEY: misc feature

; LOCATION: 15969..17969

; OTHER INFORMATION: 3'regulatory region

; NAME/KEY: allele

; LOCATION: 1239

; OTHER INFORMATION: 20-828-311 : polymorphic base C or T

; NAME/KEY: allele

; LOCATION: 12347

; OTHER INFORMATION: 17-42-319 : polymorphic base C or T

; NAME/KEY: allele

; LOCATION: 15241

; OTHER INFORMATION: 17-41-250 : polymorphic base C or T

; NAME/KEY: allele

; LOCATION: 42218

; OTHER INFORMATION: 20-841-149 : polymorphic base A or G

; NAME/KEY: allele

; LOCATION: 45442

; OTHER INFORMATION: 20-842-115 : polymorphic base A or G

; NAME/KEY: allele

; LOCATION: 77058

; OTHER INFORMATION: 20-853-415 : polymorphic base C or T

; NAME/KEY: primer_bind

; LOCATION: 929..949

; OTHER INFORMATION: 20-828.pu

; NAME/KEY: primer_bind

; LOCATION: 1357..1377

; OTHER INFORMATION: 20-828.rp complement

; NAME/KEY: primer_bind

; LOCATION: 12029..12050

; OTHER INFORMATION: 17-42.pu

; NAME/KEY: primer_bind

; LOCATION: 12581..12603

; OTHER INFORMATION: 17-42.rp complement

; NAME/KEY: primer_bind

; LOCATION: 14992..15012

; OTHER INFORMATION: 17-41.pu

; NAME/KEY: primer_bind

; LOCATION: 15460..15482

; OTHER INFORMATION: 17-41.rp complement

; NAME/KEY: primer_bind

; LOCATION: 42070..42090

; OTHER INFORMATION: 20-841.pu

; NAME/KEY: primer_bind

; LOCATION: 42572..42591

; OTHER INFORMATION: 20-841.rp complement

; NAME/KEY: primer_bind

; LOCATION: 45328..45347

; OTHER INFORMATION: 20-842.pu

; NAME/KEY: primer_bind

; LOCATION: 45863..45883

; OTHER INFORMATION: 20-842.rp complement

; NAME/KEY: primer_bind

; LOCATION: 76644..76664

; OTHER INFORMATION: 20-853.pu

; NAME/KEY: primer_bind

; LOCATION: 77166..77185

; OTHER INFORMATION: 20-853.rp complement

; NAME/KEY: primer_bind

; LOCATION: 1220..1238

; OTHER INFORMATION: 20-828-311.mis

; NAME/KEY: primer_bind

; LOCATION: 12328..12346

; OTHER INFORMATION: 17-42-319.mis

; NAME/KEY: primer_bind

; LOCATION: 12348..12366

; OTHER INFORMATION: 17-42-319.mis complement

; NAME/KEY: primer_bind

; LOCATION: 15222..15240

; OTHER INFORMATION: 17-41-250.mis

; NAME/KEY: primer_bind

; LOCATION: 15242..15260

; OTHER INFORMATION: 17-41-250.mis complement

; NAME/KEY: primer_bind

; LOCATION: 42199..42217

; OTHER INFORMATION: 20-841-149.mis

; NAME/KEY: primer_bind

LOCATION: 42219..42237
OTHER INFORMATION: 20-841-149.mis complement
NAME/KEY: primer bind
LOCATION: 45423..45441
OTHER INFORMATION: 20-842-115.mis
NAME/KEY: primer_bind
LOCATION: 45443..45461
OTHER INFORMATION: 20-842-115.mis complement
NAME/KEY: primer bind
LOCATION: 77039..77057
OTHER INFORMATION: 20-853-415.mis
NAME/KEY: primer_bind
LOCATION: 77059..77077
OTHER INFORMATION: 20-853-415.mis complement
NAME/KEY: misc binding
LOCATION: 1227..1251
OTHER INFORMATION: 20-828-311.probe
NAME/KEY: misc binding
LOCATION: 12335..12359
OTHER INFORMATION: 17-42-319.probe
NAME/KEY: misc binding
LOCATION: 15225..15253
OTHER INFORMATION: 17-41-250.probe
NAME/KEY: misc binding
LOCATION: 42206..42230
OTHER INFORMATION: 20-841-149.probe
NAME/KEY: misc binding
LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
NAME/KEY: misc binding
LOCATION: 77046..77070
OTHER INFORMATION: 20-853-415.probe
US-09-750-580-1

Query Match 2.3%; Score 42.4; DB 4; Length 81001;
Best Local Similarity 81.7%; Pred. No. 0.19;
Matches 49; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1504 TAAAGATGAGAACTCAGGCTCAGAGAGGTGAAGTACCTGCGCCCAAGGCCACAGCC 1563
DB 33792 TTAAGATAGGAACTCAGCTCAGTGAACACCTTGGCCCAAGGGTACAGCC 33733

RESULT 10
US-09-620-312D-401
Sequence 401, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yunqing
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Dmanac, Radolje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
FILE REFERENCE: 784CIP23
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725

PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_fl_genes Version 1.0
SEQ ID NO 401
LENGTH: 2697
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (135)..(1136)
US-09-620-312D-401

Query Match 2.3%; Score 42; DB 4; Length 2697;
Best Local Similarity 77.3%; Pred. No. 0.036;
Matches 51; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1508 AGATGAGAACTCAGGCTCAGAGAGGTGAAGTACCTGCGCCCAAGGCCACAGCCAGAA 1567
DB 104 AGATGAGAACTCAGGCTCAGAGAGGTGACATGCTTCTCGAGGCCGCCAGCCAGTG 163

QY 1568 TCTTCC 1573
DB 164 TGAACC 169

RESULT 11
US-09-800-960-3
Sequence 3, Application US/09800960
Patent No. 6387677
GENERAL INFORMATION:
APPLICANT: YE, Jane et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001158
CURRENT APPLICATION NUMBER: US/09/800,960
CURRENT FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Fast-SEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 62804
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(62804)
OTHER INFORMATION: n = A,T,C or G
US-09-800-960-3

Query Match 2.3%; Score 41.6; DB 4; Length 62804;
Best Local Similarity 78.1%; Pred. No. 0.28;
Matches 50; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1504 TAAAGATGAGAACTCAGGCTCAGAGAGGTGAAGTACCTGCGCCCAAGGCCACAGCC 1563
DB 36676 TTATAGATAAGAAATTGAGGCTCAGAGAGGTTAGTAAGTACCTACCAAGGTCACAGCT 36735

QY 1564 AGAA 1567
DB 36736 GGCA 36739

RESULT 12
US-08-060-925A-12
Sequence 12, Application US/08060925A
Patent No. 5439824
GENERAL INFORMATION:
APPLICANT: Brantley, Mark
APPLICANT: Laubach, Victor
TITLE OF INVENTION: INCREASED EXPRESSION OF ALPHA-1
TITLE OF INVENTION: ANTI-TRYPsin IN EXPRESSION VECTORS THROUGH THE INCLUSION OF
TITLE OF INVENTION: INTRON II
NUMBER OF SEQUENCES: 12

LOCATION: 42219..42237
OTHER INFORMATION: 20-841-149.mis complement
NAME/KEY: primer bind
LOCATION: 45423..45441
OTHER INFORMATION: 20-842-115.mis
NAME/KEY: primer_bind
LOCATION: 45443..45461
OTHER INFORMATION: 20-842-115.mis complement
NAME/KEY: primer bind
LOCATION: 77039..77057
OTHER INFORMATION: 20-853-415.mis
NAME/KEY: primer_bind
LOCATION: 77059..77077
OTHER INFORMATION: 20-853-415.mis complement
NAME/KEY: misc binding
LOCATION: 1227..1251
OTHER INFORMATION: 20-828-311.probe
NAME/KEY: misc binding
LOCATION: 12335..12359
OTHER INFORMATION: 17-42-319.probe
NAME/KEY: misc binding
LOCATION: 15225..15253
OTHER INFORMATION: 17-41-250.probe
NAME/KEY: misc binding
LOCATION: 42206..42230
OTHER INFORMATION: 20-841-149.probe
NAME/KEY: misc binding
LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
NAME/KEY: misc binding
LOCATION: 77046..77070
OTHER INFORMATION: 20-853-415.probe
US-09-750-580-1

Query Match 2.3%; Score 42.4; DB 4; Length 81001;
Best Local Similarity 81.7%; Pred. No. 0.19;
Matches 49; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1504 TAAAGATGAGAACTCAGGCTCAGAGAGGTGAAGTACCTGCGCCCAAGGCCACAGCC 1563
DB 33792 TTAAGATAGGAACTCAGCTCAGTGAACACCTTGGCCCAAGGGTACAGCC 33733

RESULT 10
US-09-620-312D-401
Sequence 401, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yunqing
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Dmanac, Radolje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
FILE REFERENCE: 784CIP23
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
; STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
; CITY: NEWPORT BEACH
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/060,925A
; FILING DATE: 06-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fuller, Michael L.
; REGISTRATION NUMBER: 36,516
; REFERENCE/DOCKET NUMBER: NIH040.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10627 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-060-925A-12

Query Match 2.3%; Score 41; DB 1; Length 10627;
Best Local Similarity 82.5%; Pred. No. 0.16;
Matches 47; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

2y 1513 AGGAACCTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGCAATC 1569
Db 1687 AGGAACCTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGCAATC 1743

RESULT 13
US-09-918-686-2/c
; Sequence 2, Application US/09918686
; Patent No. 6475739
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary
; APPLICANT: Proll, Sean
; APPLICANT: Paepfer, Bryan
; APPLICANT: Staehling-Hampton, Karen
; TITLE OF INVENTION: METHODS FOR IDENTIFYING
; TITLE OF INVENTION: GENOMIC DELETIONS
; FILE REFERENCE: 240083.515
; CURRENT APPLICATION NUMBER: US/09/918,686
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 51719
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1246..2572, 2604
; OTHER INFORMATION: n = A,T,C or G
US-09-918-686-2

Query Match 2.3%; Score 41; DB 4; Length 51719;
Best Local Similarity 76.9%; Pred. No. 0.38;
Matches 50; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
; STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
; CITY: NEWPORT BEACH
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/918,686
; FILING DATE: 06-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fuller, Michael L.
; REGISTRATION NUMBER: 36,516
; REFERENCE/DOCKET NUMBER: NIH040.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92139
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 7043, 8369, 8401
; OTHER INFORMATION: n = A,T,C or G
US-09-918-686-1

Query Match 2.3%; Score 41; DB 4; Length 92139;
Best Local Similarity 76.9%; Pred. No. 0.52;
Matches 50; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1507 AAGATGAGGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGCA 1566
Db 41491 AAGATGAGGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGCA 41432

Qy 1567 ATCTT 1571
Db 41431 AAATT 41427

RESULT 14
US-09-918-686-1/c
; Sequence 1, Application US/09918686
; Patent No. 6475739
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary
; APPLICANT: Proll, Sean
; APPLICANT: Paepfer, Bryan
; APPLICANT: Staehling-Hampton, Karen
; TITLE OF INVENTION: METHODS FOR IDENTIFYING
; TITLE OF INVENTION: GENOMIC DELETIONS
; FILE REFERENCE: 240083.515
; CURRENT APPLICATION NUMBER: US/09/918,686
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 92139
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 7043, 8369, 8401
; OTHER INFORMATION: n = A,T,C or G
US-09-918-686-1

Query Match 2.3%; Score 41; DB 4; Length 92139;
Best Local Similarity 76.9%; Pred. No. 0.52;
Matches 50; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1507 AAGATGAGGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGCA 1566
Db 47288 AAGATGAGGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGCA 47229

Qy 1567 ATCTT 1571
Db 47228 AAATT 47224

RESULT 15
US-09-820-005-3
; Sequence 3, Application US/09820005
; Patent No. 6489149
; GENERAL INFORMATION:
; APPLICANT: SHAO, Wei et al
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001198
; CURRENT APPLICATION NUMBER: US/09/820,005
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 18853
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(18853)
; OTHER INFORMATION: n = A,T,C or G
US-09-820-005-3

Query Match 2.2%; Score 40.8; DB 4; Length 18853;

RESULT 19
US-08-033-081E-2/c

OTHER INFORMATION: n = A, T, C or G
US-09-918-686-1

Sequence 2, Application US/08033081B
Patent No. 5498521
GENERAL INFORMATION:
APPLICANT: Dryja, Thaddeus P.
APPLICANT: Berison, Elliot L.
TITLE OF INVENTION: DIAGNOSIS OF HEREDITARY RETINAL
TITLE OF INVENTION: DEGENERATIVE DISEASES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/033,081B
FILING DATE: March 11, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/825,296
FILING DATE: January 23, 1992
APPLICATION NUMBER: 07/469,215
FILING DATE: January 24, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/069005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6953
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
IS-08-033-081B-2
Query Match 2.2%; Score 40.6; DB 1; Length 6953;
Best Local Similarity 64.2%; Pred. No. 0.16;
Matches 61; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
Y 1480 TGGAGATCTACCTCTGGAGCTGTTAAAGATGAGGAACTCAGGCTCAGAGAGGTGAG 1539
b 4882 TGGTGTGTTTGCCCTTTCTACCTTTCTATGATGAGGAACTCAAGCAAGCAAGGAAAT 4823
Y 1540 TACTGCCCCAAGGCCACACAGCCAGCAATCTTCCA 1574
b 4822 TGACTTCCAGGCCCATACAGCTAGAAAATGGCA 4788
RESULT 20
US-09-816-094-3/c
Sequence 3, Application US/09816094
Patent No. 6534299
GENERAL INFORMATION:
APPLICANT: Wei, Ming-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL000536-CIP
CURRENT APPLICATION NUMBER: US/09/816,094
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3

LENGTH: 7301
TYPE: DNA
ORGANISM: Human
US-09-816-094-3
Query Match 2.2%; Score 40.6; DB 4; Length 7301;
Best Local Similarity 73.2%; Pred. No. 0.17; Indels 0; Gaps 0;
Matches 52; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Y 1504 TAAAGATGAGGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGCCACACAGCC 1563
b 1813 TTACAGAGAGGAGCTCTGAAGCACAGAGAGGTGAAGTCACTTGTCTGAGGTCAACAGCA 1754
Y 1564 AGAATCTTCCA 1574
b 1753 AGCAAGTAACA 1743
RESULT 21
US-09-301-665-3
Sequence 3, Application US/09301665
Patent No. 6207876
GENERAL INFORMATION:
APPLICANT: KELLEMS, RODNEY E.
APPLICANT: DATTA, SURJIT K.
APPLICANT: BLACKBURN, MICHAEL R.
TITLE OF INVENTION: ADENOSINE DEAMINASE DEFICIENT TRANSGENIC MICE AND
TITLE OF INVENTION: METHODS FOR THE USE THEREOF
FILE REFERENCE: JPH-243
CURRENT APPLICATION NUMBER: US/09/301,665
CURRENT FILING DATE: 1999-04-28
EARLIER APPLICATION NUMBER: 60/083,408
EARLIER FILING DATE: 1998-04-29
EARLIER APPLICATION NUMBER: 60/083,370
EARLIER FILING DATE: 1998-04-28
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 36741
TYPE: DNA
ORGANISM: Homo sapiens
US-09-301-665-3
Query Match 2.2%; Score 40.6; DB 3; Length 36741;
Best Local Similarity 83.6%; Pred. No. 0.41; Indels 0; Gaps 0;
Matches 46; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Y 1508 AGATGAGGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGCCACACAGC 1562
b 18218 AGTTGAGGAACTGAGGCTCAGAGAGGTCAAGTGTCTTGTCTGAGGTCAACAGC 18272
RESULT 22
US-09-146-053-3/c
Sequence 3, Application US/09146053A
Patent No. 6399349
GENERAL INFORMATION:
APPLICANT: Ryan, James W.
APPLICANT: Sprinkle, Terry Joe Curtis
APPLICANT: Venema, Richard C.
TITLE OF INVENTION: Human Aminopeptidase P Gene
FILE REFERENCE: MCG103
CURRENT APPLICATION NUMBER: US/09/146,053A
CURRENT FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/057,854
EARLIER FILING DATE: 1997-09-02
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 50000
TYPE: DNA
ORGANISM: Homo sapiens
US-09-146-053-3

Query Match 2.2%; Score 40.6; DB 4; Length 50000;
Best Local Similarity 73.2%; Pred. No. 0.49;
Matches 52; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1504 TAAAGATGAGAACTGAGGCTCAGAGAGGTGAAGTACTGCGCCCAAGGCCACACAGCC 1563
DB 14909 TTACATCTGAGGAACTGAGGTTTCAAGAGGGGCGAGTACTTATTCAAGTCAACAGCT 14850

QY 1564 AGAATCTTCCA 1574
DB 14849 AGGATGTCCA 14839

RESULT 23
US-09-491-356C-1/c
; Sequence 1, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Ginis, Edward I.
; APPLICANT: Delisi, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
; FILE REFERENCE: 9465.6US11
; CURRENT APPLICATION NUMBER: US/09/491,356C
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083,465
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 55298
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (485)..(485)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (838)..(838)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (16728)..(16728)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (22750)..(22750)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (22756)..(22756)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (28519)..(28519)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (44804)..(44804)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (45002)..(45002)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (54049)..(54049)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (54226)..(54226)
; OTHER INFORMATION: n is not determined
; OTHER INFORMATION: n is not determined
US-09-491-356C-1

Query Match 2.2%; Score 40.6; DB 4; Length 55298;
Best Local Similarity 73.2%; Pred. No. 0.51;
Matches 52; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1504 TAAAGATGAGAACTGAGGCTCAGAGAGGTGAAGTACTGCGCCCAAGGCCACACAGCC 1563
DB 35231 TCACGTGATGGGAAACTGAGGTTTCAAGGGGTAAAGTGACTTCTCAAGATCACACAGCT 35172

QY 1564 AGAATCTTCCA 1574
DB 35171 AGGAAGTGCTA 35161

RESULT 24
US-09-220-132-182
; Sequence 182, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
; APPLICANT: Shytjan, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
; OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 07334-074001
; CURRENT APPLICATION NUMBER: US/09/220,132
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/068,821
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 1601
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-220-132-182

Query Match 2.2%; Score 40.4; DB 4; Length 1601;
Best Local Similarity 75.8%; Pred. No. 0.081;
Matches 50; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1504 TAAAGATGAGAACTGAGGCTCAGAGAGGTGAAGTACTGCGCCCAAGGCCACACAGCC 1563
DB 181 TACAAGACAGGGAGAGCTGAAGACACAGAGAGGTAAAGTGACTTGCCCAAGGTCACACAGTT 240

QY 1564 AGAATC 1569
DB 241 AAATTC 246

RESULT 25
US-09-146-053-5/c
; Sequence 5, Application US/09146053A
; Patent No. 6399349
; GENERAL INFORMATION:
; APPLICANT: Ryan, James W.
; APPLICANT: Sprinkle, Terry Joe Curtis
; APPLICANT: Venema, Richard C.
; TITLE OF INVENTION: Human Aminopeptidase P Gene
; FILE REFERENCE: MCG103
; CURRENT APPLICATION NUMBER: US/09/146,053A
; CURRENT FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/057,854
; EARLIER FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 44453
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-146-053-5

Query Match 2.2%; Score 39.6; DB 4; Length 44453;
Best Local Similarity 77.4%; Pred. No. 0.9;
Matches 48; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1504 TAAAGATGAGAACTGAGGCTCAGAGAGGTGAAGTACTGCGCCCAAGGCCACACAGCC 1563

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1b 31158 TTACAGAGAAGAACTGAAGCACAAGAAAGCTTGAAGCACTTGCCCAAGGCCAAACAGCC 31098
Y 1564 AG 1565
b 31098 AG 31097

RESULT 26
US-09-328-111-672/c
Sequence 672, Application US/09328111
Patent No. 6262333
GENERAL INFORMATION:
APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, Jon H.
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Catino, Theodore J.
APPLICANT: Derti, Adnan
APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 672
LENGTH: 377
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(377)
OTHER INFORMATION: n = A,T,C or G
US-09-328-111-672

Query Match 2.2%; Score 39.2; DB 3; Length 377;
Best Local Similarity 78.3%; Pred. No. 0.082;
Matches 47; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Y 1508 AGATGAGAAACTCAGGCTCAGAGAGGGAAGTACTGGCCCAAGGCCACACAGCCAGAA 1567
b 180 AGATGAGAAACTCAGGTTTCAGAGAGGCCACTTGGCTTGCCCAAGTTCACACAGCGGGA 121

RESULT 27
US-08-467-155A-2/c
Sequence 2, Application US/08467155A
Patent No. 5736377
GENERAL INFORMATION:
APPLICANT: Band, Vimla
TITLE OF INVENTION: NBS-1 POLYPEPTIDES, DNA, AND RELATED
TITLE OF INVENTION: MOLECULES AND METHODS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0. Version #1.30

```


APPLICATION NUMBER: US/07/935,313
FILING DATE: 26-AUG-1991
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PT29pt-F's
S-08-232-463-14

Query Match 2.2%; Score 39.2; DB 1; Length 7218;
Best Local Similarity 7.0%; Pred. No. 0.43; Mismatches 184; Indels 0; Gaps 0;
Matches 29; Conservative 201; Mismatches 184; Indels 0; Gaps 0;

Y 490 TTTTCCATGGAAGAGATATCTCCCGCGGAGAGCTGGCACCCTACTTGGAGCCACAG 549
b 997 TTTTCTCTGTTTGGCATACCTCACAGAAATATTCGAGCTTGGCTGCAGTTCAGGG 1056
Y 550 GCTGTAGTACTGCTCGCTGTACTCTCAGAGGGCGCCCACTGAGTGTCTTACCGCC 609
b 1057 AGCTTGGAT 1116
Y 610 TCACCTGTCGCTGTCCACTGCGCCGACGCTGTGACGAGCCACGAGCAATCTGTCCA 669
b 1117 YY 1176
Y 670 AGTGTGGAACTCACACTCCCTCTGACTCCGCGCCGCCACCAAGTCTCCAGCACA 729
b 1177 YY 1236
Y 730 ACGGACCATGTACCAACAGCAGAGATCTTCAGTGCCCATGAGCTGTCCCTCCCGCC 789
b 1237 YY 1296
Y 790 TGCCCAACCATGTGCTCTGCTGAGCTGCACAGAGGCGCATCTACTGCGGCCTCACAA 849
b 1297 YY 1356
Y 850 CTGCGCCGCAACAGGCTGCCAGACCCCTCCGCTGCCAGACTCTGCTGCC 903
b 1357 YY 1410

RESULT 32
US-09-740-027-3/c
Sequence 3, Application US/09740027
Patent No. 6485939
GENERAL INFORMATION:
APPLICANT: YE, Jane et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER COFACTOR
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER
TITLE OF INVENTION: COFACTOR PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001052
CURRENT APPLICATION NUMBER: US/09/740,027
CURRENT FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 24707
TYPE: DNA
ORGANISM: Human

US-09-740-027-3
Query Match 2.2%; Score 39.2; DB 4; Length 24707;
Best Local Similarity 78.3%; Pred. No. 0.85;
Matches 47; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1508 AGATGAGAAACTGAGCTCAGAGAGTGAAGTACTGCGCCCAAGCCACACAGCCAGAA 1567
Db 13256 AGATGGGAAACTGAGCTCAGAGATGTGGAGCCCACTGCTGACATCACAGCCAGAA 13197

RESULT 33
US-08-343-760A-1
Sequence 1, Application US/08343760A
Patent No. 5679783
GENERAL INFORMATION:
APPLICANT: De Robertis, Edward M
APPLICANT: Sasai, Yoshiki
TITLE OF INVENTION: Tissue Differentiation Affecting
TITLE OF INVENTION: Factor and Composition
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hsue
STREET: Four Embarcadero Center, Suite 1450
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/343,760A
APPLICATION NUMBER: US/08/343,760A
FILING DATE: 22-NOV-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Siebert, J. Suzanne
REGISTRATION NUMBER: 28,758
REFERENCE/DOCKET NUMBER: 3100.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 363-5556
TELEFAX: (415) 362-5418
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3796 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-343-760A-1

Query Match 2.1%; Score 39; DB 1; Length 3796;
Best Local Similarity 65.5%; Pred. No. 0.34;
Matches 57; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 594 GTGATGTTTACCGCTCCACTGTCGCTGTCCACTGCGCCAGCCTGTGACGAGCCAA 653
Db 2466 GTGATTTGTATCTTATTTGTGTGCGCCACTCTGAACTGCTCCAGCCTGTCCATTGGCCA 2525

QY 654 CAGCAATGCTGTCCCAAGTGTGTGAA 680
Db 2526 GATCAGTGTCTCTCTGTGTGTGAA 2552

RESULT 34
US-08-927-219-130
Sequence 130, Application US/08927219
Patent No. 6187533
GENERAL INFORMATION:
APPLICANT: Bell, Graeme I.
APPLICANT: Yamagata, Kazuya

APPLICANT: Oda, Naohisha
APPLICANT: Kaisaki, Pamela J.
APPLICANT: Furuca, Hiroto
APPLICANT: Horikawa, Yukio
APPLICANT: Menzel, Stephen
TITLE OF INVENTION: MUTATIONS IN THE DIABETES SUSCEPTIBILITY
TITLE OF INVENTION: GENES HEPATOCYTE NUCLEAR FACTOR (HNF) 1 ALPHA, HNF-1BETA
TITLE OF INVENTION: AND HNF-4ALPHA
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,219
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,679
FILING DATE: 30-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,056
FILING DATE: 02-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/025,719
FILING DATE: 10-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:272
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 130:
SEQUENCE CHARACTERISTICS:
LENGTH: 10014 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-927-219-130
Query Match 2.1%; Score 39; DB 3; Length 10014;
Best Local Similarity 71.8%; Pred. No. 0.59;
Matches 51; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
Qy 1504 TAAAGATGAGGAACTGAGGCTCAGAGAGTGAAGTACCTGGCCCAAGGCCACACAGCC 1563
Db 5408 TCATAGGTGAGGAGATGGGGCACAGAGAGTTAAGTAACTGTCTCAAGGTCAATAGCT 5467
Qy 1564 AGAATCTTCCA 1574
Db 5468 ACTATCCAGCA 5478
RESULT 35
US-09-288-143-59/c
Sequence 59, Application US/09288143
Patent No. 6433139
GENERAL INFORMATION:
APPLICANT: Brewer et al.
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REFERENCE: P2018P1
CURRENT APPLICATION NUMBER: US/09/288,143
CURRENT FILING DATE: 1999-04-08
EARLIER APPLICATION NUMBER: PCT/US98/21142

EARLIER FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: 60/061,463
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061,529
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/071,498
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061,527
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061,536
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061,532
EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 219
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 59
LENGTH: 441
TYPE: DNA
ORGANISM: Homo sapiens
US-09-288-143-59
Query Match 2.1%; Score 38.8; DB 4; Length 441;
Best Local Similarity 79.3%; Pred. No. 0.12;
Matches 46; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Qy 1508 AGATGAGGAACTGAGGCTCAGAGAGTGAAGTACCTGGCCCAAGGCCACACAGCCAG 1565
Db 129 AAATCAGAAATGTGGCACAGAGAGTTAAGTACTTGGCCCAAGGTCAACAGCTAG 72
RESULT 36
US-08-756-506-1
Sequence 1, Application US/08756506
Patent No. 5905185
GENERAL INFORMATION:
APPLICANT: Garner, Ian
APPLICANT: Cottingham, Ian R.
APPLICANT: Temperley, Simon M.
APPLICANT: Foster, Donald C.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Prunkard, Donna E.
TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
TITLE OF INVENTION: ANIMALS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,506
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 95-28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11725 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: join(3520..3630, 5093..5117, 5210..5347, 5450
LOCATION: ..5584, 8253..8395, 9269..9386, 10516..11102)
US-08-756-506-1

Query Match 2.1%; Score 38.8; DB 2; Length 11725;
Best Local Similarity 58.8%; Pred. No. 0.74;
Matches 67; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

2y 1448 CTTTGGCCCTGACACGAGGCTCGACTGCTGGAGATCTACCTCTGGAAGCTGTTAA 1507
3095 CTTATCTCTGGCCAGGCTGTATGATGTTTACATGACGGTCTATCCCCATGTTTT 3154

2y 1508 AGATCAGAAACTAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAG 1561
3155 GGATGAGTAATTGAACTTAGAAGGTAAAGACACTGGCTCAGGTCACACAG 3208

RESULT 37
US-08-370-319C-12/c
Sequence 12 Application US/08370319C
Patent No. 5856091
GENERAL INFORMATION:
APPLICANT: Brichard, Vincent; Van Pel, Aline;
APPLICANT: Traversari, Catia; W Ifel, Thomas; Coullie, Pierre;
APPLICANT: Boon-Falleur, Thierry; De Plaeen, Etienne
TITLE OF INVENTION: ISOLATED NUCLEIC ACID SEQUENCE CODING FOR A
TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PERCURSOR PROCESSED TO AT LEAST ONE TU
TITLE OF INVENTION: REJECTION ANTIGEN PRESENTED BY HLA-A2
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,319C
FILING DATE: 10-JANUARY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/272,351
FILING DATE: 8-JULY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/032,978
FILING DATE: 18-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5856091man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5377.1
TELEPHONE: (212) 688-9200
TELEFAX: (212) 688-9200
SEQUENCE CHARACTERISTICS:
LENGTH: 4129 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: The sequence is preceded by an
OTHER INFORMATION: unsequenced portion of from 4.7 to 5.3
US-08-370-319C-12

Query Match 2.1%; Score 38.6; DB 2; Length 4129;
Best Local Similarity 72.5%; Pred. No. 0.47;
Matches 50; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1503 GTAAAGATGAGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGC 1562
Db 3342 GTTACAGAAATGGGAACCTGGGACACAGAGGTTAACTCGCTTGGCCATGGTCACACAAC 3283

Qy 1563 CAGATCTT 1571
Db 3282 TAGTAAGTT 3274

RESULT 38
US-09-224-834-12/c
Sequence 12 Application US/09224834
Patent No. 6201111
GENERAL INFORMATION:
APPLICANT: Brichard, Vincent; Van Pel, Aline;
APPLICANT: Traversari, Catia; W Ifel, Thomas; Coullie, Pierre;
APPLICANT: Boon-Falleur, Thierry; De Plaeen, Etienne
TITLE OF INVENTION: ISOLATED NUCLEIC ACID SEQUENCE CODING FOR A
TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PERCURSOR PROCESSED TO AT LEAST ONE TU
TITLE OF INVENTION: REJECTION ANTIGEN PRESENTED BY HLA-A2
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,834
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/370,319
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/032,978
FILING DATE: 18-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6201111man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5377.1
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 4129 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: The sequence is preceded by an
OTHER INFORMATION: unsequenced portion of from 4.7 to 5.3
US-09-224-834-12

Query Match 2.1%; Score 38.6; DB 3; Length 4129;
Best Local Similarity 72.5%; Pred. No. 0.47;
Matches 50; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1503 GTAAAGATGAGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGC 1562
Db 3342 GTTACAGAAATGGGAACCTGGGACACAGAGGTTAACTCGCTTGGCCATGGTCACACAAC 3283

QY 1468 CCTCGGACTTTGGTGGAGATCTAC-CTCTGGAAGCTGGTAAAGATGAGGAACTGAGGCT 1526
Db 53459 CACCGCTCCCGGCAGTGATAGACGTTCTTATCCCGCTGGCAGGTGAGGAGACTGATGCT 53400
QY 1527 CAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAA 1567
Db 53399 CAGGCTGGTTAAGTGACAGGCAACAAGGCCACACACCTAGGA 53359

Search completed: January 31, 2004, 04:01:41
Job time : 120 secs

2Y 1563 CAGAACTTT 1571
Db 3282 TAGTAGTT 3274
RESULT 39
JS-09-146-053-4/c
; Sequence 4, Application US/09146053A
; Patent No. 6399349
; GENERAL INFORMATION:
; APPLICANT: Ryan, James W.
; APPLICANT: Sprinkle, Terry Joe Curtis
; APPLICANT: Venema, Richard C.
; TITLE OF INVENTION: Human Aminopeptidase P Gene
; FILE REFERENCE: MCGL03
; CURRENT APPLICATION NUMBER: US/09/146,053A
; CURRENT FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/057,854
; EARLIER FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 50000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-146-053-4

Query Match 2.1%; Score 38.6; DB 4; Length 50000;
Best Local Similarity 77.0%; Pred. No. 1.9;
Matches 47; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 1504 TAAAGATGAGGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCC 1563
Db 14773 TAACAGAGGAAAAAAGTACGCTCAGAGAGAGCTGAATAACTTGCCCAAGGTCAACAGCT 14714
QY 1564 A 1564
Db 14713 A 14713

RESULT 40
US-09-754-250-3/c
; Sequence 3, Application US/09754250
; Patent No. 6376225
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001063
; CURRENT APPLICATION NUMBER: US/09/754,250
; CURRENT FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 111282
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(111282)
; OTHER INFORMATION: n = A,T,C or G
US-09-754-250-3

Query Match 2.1%; Score 38.6; DB 4; Length 111282;
Best Local Similarity 56.5%; Pred. No. 3;
Matches 91; Conservative 0; Mismatches 69; Indels 1; Gaps 1;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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un on: January 31, 2004, 00:43:14 ; Search time 3965 Seconds
(without alignments)

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aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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12: gb_est3:*

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19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_man:*

23: em_gss_mus:*

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27: em_gss_vrt:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB	ID	Description
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2	733.2	40.4	1485	11	AK007577	AK007577 Mus muscu
3	591.4	32.5	601	9	A1739159	A1739159 w118h06.x
4	479.4	26.4	481	13	EX091758	EX091758 EX091758

5	428.2	23.6	545	12	BI774183	BI774183 466194 MA
6	422.4	23.2	756	12	BI112782	BI112782 602998795
7	406.8	22.4	424	9	AL047873	AL047873 DKFZP586M
8	405.8	22.3	768	12	BI113110	BI113110 602898895
9	389.8	21.5	915	10	BE911015	BE911015 601662108
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ALIGNMENTS

RESULT 1
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LOCUS Homo sapiens FKSG37 (FKSG37) mRNA, complete cds.
DEFINITION
ACCESSION AF332891
VERSION AF332891.1 GI:12276190
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 1047)
Wang,Y.-G. and Gong,L.
Cloning of FKSG37, a novel gene located on human chromosome 11q14

AUTHORS
TITLE
JOURNAL
Unpublished

REFERENCE
2 (bases 1 to 1047)
Wang,Y.-G.

AUTHORS
TITLE
JOURNAL
Direct Submission

Submitted (01-JAN-2001) Beijing Fengkesheng Function Gene
Technology Ltd., 4 Toutiao Lu Chang Street, Xuanwu District,
Beijing 100050, P.R. China

Location/Qualifiers
1. 1047

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Query Match      43.5%; Score 790.4; DB 11; Length 1047;
Best Local Similarity 94.6%; Pred. No. 1.1e-197;
Matches 831; Conservative 0; Mismatches 41; Indels 6; Gaps 1;
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2b 21 GCAGTTGTAGGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTTCACACTCCCTCTGG 80
2Y 698 ACTCCGGCCCCACAAAGTCTCTGCAGCACAAACGGACCATGTATCAACACAGAGAT 757
2b 81 ACTCCGGCCCCACAAAGTCTCTGCAGCACAAACGGACCATGTATCAACACAGAGAT 140
2Y 758 CTTGAGTCCCATGAGCTGTTCCTCCCTCCCGCTGCCCAACCATGTGTCTCTGCAGCTG 817
2b 141 CTTGAGTCCCATGAGCTGTTCCTCCCTCCCGCTGCCCAACCATGTGTCTCTGCAGCTG 200
2Y 818 CACAGAGGCCAGATCTACTGGGCTCACAGCTGCCCGACCAAGCTGCCAGCACC 877
2b 201 CACAGAGGCCAGATCTACTGGGCTCACAGCTGCCCGACCAAGCTGCCAGCACC 260
2Y 878 CTTCCCGTGCAGACTCTCTGCTGCAAGCTGCAAGAGTGAAGCA-----GTGAGCA 931
2b 261 CTTCCCGTGCAGACTCTCTGCTGCAAGCTGCAAGAGTGAAGCTGCTGCTGCTGCTGCT 320
2Y 932 ATCGGATGAAGAGGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 991
2b 321 ATGCTCAGTCACTGACTTTCATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 380
2Y 992 TTCAGTATGCTGGGAGAAAGAGAGGCGCGGCGCACCCAGCCCCCACTGCTGCTGCTGCTGCTGCT 1051
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2Y 1052 CCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1111
2b 441 CCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 500
2Y 1112 GATCGTCTGAAGGAGAAACATGAAGAGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1171
2b 501 GATCGTCTGAAGGAGAAACATGAAGAGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 560
2Y 1172 CGGGAGGTGTGGCACCCGCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1231
2b 561 CGGGAGGTGTGGCACCCGCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 620
2Y 1232 CTGTGAGGATGGCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1291
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2Y 1292 TCACCCCGAGAAAGTGGTGGGAGTCTGCTGAGATTTGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1351
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2Y 1352 TGGCCACAGTGAGATCAGTTCTTACCAAGTGTCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1411
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RESULT 2
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LOCUS Mus musculus 10 day old male pancreas cDNA, RIKEN full-length
DEFINITION musclic library, clone:1810022C01 product:CHORDIN-RELATED PROTEIN
NEURALIN-2 homolog [Mus musculus], full insert sequence.
AK007577 GI:12841206
VERSION HTC; CAP trapper.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci, P., and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M.,
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G.,
Quackenbush, J., Schriml, L.M., Stauber, F., Suzuki, R., Tomita, M.,
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Butt, C.,
Fletcher, M., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Hofmann, C., Hume, D.A., Kaniwa, M., Lee, N.H., Lyons, P.,
Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,
Toyo-oka, K., Wang, K.H., Weitz, C., Wittaker, C., Wilm, L.,
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
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TITLE
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AUTHORS
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Db 1273 AAGATTTCAGAAAGAGGCTCAGAACTTCGGCTGCTCACCAGCCAGGAGTGCAGAGGTTACT 1332
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RESULT 3
LOCUS AI739159/c
DEFINITION w18h06.x1 NCI CGAP Col6 Homo sapiens cDNA clone IMAGE:2390651 3', similar to SN:GAL1_CHICK P02457 PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.; mRNA sequence.

ACCESSION AI739159
VERSION AI739159.1 GI:5101140
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 601)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
cDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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High quality sequence stop: 445.
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/note="Organ: Colon; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP Col6 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 113 a 152 c 167 g 169 t
ORIGIN

Query Match 32.5%; Score 591.4; DB 9; Length 601;
Best Local Similarity 99.0%; Pred. No. 3.8e-145;
Matches 595; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db 601 CCATGCATCTATGCACCTGTGAGGATGGCGCCAGGAGTGCAGAGGTTGACCTGTCCC 542
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Db 121 GAAGGTCAAGGCTCAGAGTCCAGACAAAGTGCACCAAGACATACCAAGACCTAACAGTTGCAG 62
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1815 A 1815
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RESULT 4
LOCUS BX091758
DEFINITION BX091758 Soares testis NHT Homo sapiens cDNA clone IMAGE:998H054492
ACCESSION BX091758
VERSION BX091758.1 GI:27824968
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 481)
Ebert, I., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.
Human Unigeneset - RZPD3
Unpublished
Contact: Ina Rofls
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGP998H054492.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
<http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972>
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de

Db	30
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QY	1020	CCGGGACCCAGCCCGCCCTGCGCT <th>CAGCGCCCTCTGAGCTTCATCCTCGCCACTTC</th> <td>1079</td>	CAGCGCCCTCTGAGCTTCATCCTCGCCACTTC	1079	
Db	478	CCAGCAGCCAGCCCGCCCTGCGCT <th>CAGCTCCCTCTGGGCTTCATCCTCGCCACTTC</th> <td>537</td>	CAGCTCCCTCTGGGCTTCATCCTCGCCACTTC	537	
QY	1080	AGACCCAAAGGAGCAGGACGACAA <th>CTGTCAGATCGTCTGAAGAGAGAAACATAAGAA</th> <td>1139</td>	CTGTCAGATCGTCTGAAGAGAGAAACATAAGAA	1139	
Db	538	CAGTCAGTGAATGGGACGACCAAC <th>ATCCTGAGATTCCTGAGAGAAACATAAGAA</th> <td>597</td>	ATCCTGAGATTCCTGAGAGAAACATAAGAA	597	
QY	1140	GCCTGTGTGATGGCGGGAAGACGT <th>ACTCTCCAGGGAGGTGTGGACCCGGCCTTC</th> <td>1199</td>	ACTCTCCAGGGAGGTGTGGACCCGGCCTTC	1199	
Db	598	GCTTGCACACAAATGGGAAGACA <th>TACTCCATGGGAGGTGTGGACCCCACTGTGCTC</th> <td>657</td>	TACTCCATGGGAGGTGTGGACCCCACTGTGCTC	657	
QY	1200	GCCTTCGGCCCTTGCCCTGCATCT <th>ATGACCTGAGGATGGCGCCAGAGCTGCCA</th> <td>1258</td>	ATGACCTGAGGATGGCGCCAGAGCTGCCA	1258	
Db	658	TCCTTTGGCCCATGCGCTGCATCT <th>GTGCAATGTATCGATGGTACCGAGCTGCCA</th> <td>717</td>	GTGCAATGTATCGATGGTACCGAGCTGCCA	717	
QY	1259	GGTGTGACCTGTCCACCGAGTACC <td>1284</td> <td></td>	1284		
Db	718	-CGTGTGAATGGCCCAACCAATAT <td>CC 742</td> <td></td>	CC 742		
RESULT 7	AL047873	424 bp	mrna	linear	EST 01-MAR-2000
LOCUS	DKFZp586M2422.r1.586	(synonym: hute1)	Homo sapiens	cdna	clone
DEFINITION	DKFZp586M2422, mRNA sequence.				
ACCESSION	AL047873				
VERSION	AL047873.1	GI:4728061			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 424)				
TITLE	Koehler, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.				
JOURNAL	EST (Koehler, et al.)				
COMMENT	Unpublished				
	Contact: Koehler K				
	IMPS				
	Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany				
	This is the 5' sequence of the clone insert				
	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer				
	Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;				
	sequenced by BMF (Biomedical Research Center at the Charite,				
	Berlin/Germany) within the cdna sequencing consortium of the German				
	Genome Project.				
	No sl sequence available.				
	This clone (DKFZp586M2422) is available at the RZPD in Berlin.				

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

Location/Qualifiers
1. .424
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DXFp586M2422"
/tissue_type="uterus"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="386 (synonym: hutel)"
/note="Vector: pSPort1; Site_1: NotI; Site_2: SalI/MluI"
BASE COUNT 140 a 108 c 96 g 80 t

Query Match 22.4%; Score 406.8; DB 9; Length 424;
Best Local Similarity 99.5%; Pred. No. 2.2e-96;
Matches 408; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1408 TCACACATCGGTATCCCGAGCCAGACACCTGCGTTCGCTTGGGACACGAGG 1467
1468 CTTGCGACTTGGTGGAGATCTACCTCTGGAAGCTGTTAAAGATGAGGAACCTGAGGCTC 1527
61 CTTGCGACTTGGTGGAGATCTACCTCTGGAAGCTGTTAAAGATGAGGAACCTGAGGCTC 120
1528 AGAGAGGTGAAGTACCTGGCGCCAGGCGCACAGCCAGATCTTCCACTTGACTCAGATC 1587
121 AGAGAGGTGAAGTACCTGGCGCCAGGCGCACAGCCAGATCTTCCACTTGACTCAGATC 180
1588 AGAAGAGTGAAGAGAGAGTCCAGAGAGGACAGAGTTCGACTGCTCGTGGC 1647
181 AGAAGAGTGAAGAGAGAGTCCAGAGAGGACAGAGTTCGACTGCTCGTGGC 240
1648 CCCAGAGAGTCACTGGAAGCTTCTAGCCAGAGCCCTGGAGCTGAAGTCAAGGCC 1707
241 CCCAGAGAGTCACTGGAAGCTTCTAGCCAGAGCCCTGGAGCTGAAGTCAAGGCC 300
1708 AGTCCAGAGAGTGAAGAGAGATCAAGAGAGCTTAAGAGTTCAGATGATGATGAT 1767
301 AGTCCAGAGAGTGAAGAGAGATCAAGAGAGCTTAAGAGTTCAGATGATGATGAT 360
1768 AATTGTTGTTATTATATATATTAATAAATAAGAGTTCAGATGATGATGATGAT 1817
361 AATTGTTGTTATTATATATATTAATAAATAAGAGTTCAGATGATGATGATGAT 410

RESULT 8

1113110 768 bp mRNA linear EST 26-JUN-2001
60289895F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5028694 5',
mRNA sequence.
1113110
1113110.1 GI:14564011
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 768)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: L1AM1080 row: n column: 23
High quality sequence start: 16
High quality sequence stop: 709.

FEATURES

Location/Qualifiers
1. .768
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5028694"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

BASE COUNT 185 a 243 c 186 g 154 t

Query Match 22.3%; Score 405.8; DB 12; Length 768;
Best Local Similarity 74.4%; Pred. No. 5.3e-96;
Matches 556; Conservative 0; Mismatches 177; Indels 14; Gaps 3;

547 AAGCCTGATGTACTGCTGCGCTGTACTGCTCAGAGGGGCCCATGTGAGTTGTACC 606
16 AAGCGCGATATATGCGTGGCTGTACTGCTGTGAGAATGGACATGTGAGTTGTACC 75
607 GCCTCCACTGTCGCTGCTCCACTGCCCCAGCGCTGTGACGAGGCCACAGCAATGCTGTC 666
76 GTCTCCGCTGCCACCCCTTCACTGCTCAGAGCTGTGATGAGGCCACAGCAATGCTGTC 135
667 CCAAGTGTGGAACCTCACACTCCCTCTGGAATCCGGGCCCCACCAAGTCTGTCGAGC 726
136 CAGGTGTGTGATCTCTCATGTCCCTCTGGCTCCGAGTTCCTCTAAAGTCTGCCAGC 195
727 ACAACGGGACCATGTACCAACACAGGAGATCTTCAG-TGCCCATGAGCTGTTCCCTCC 785
196 TCAATGAGACACATACCAACATGGAGAGATCTTCAGATGCCAGGAGCTGTTCCCTGCC 255
786 CGCTGCGCCACACAGTGTCTCTGAGCTGACAGAGGGCCAGATCTACTGCGGCTC 845
256 CGGTGTCCAAACAGTGTCTCTGTGAGTGTATTGAAGGCCACACTTACTGTGCTCTC 315
846 ACACTGCGCCGAGAACAGAGCTGCCAGCCCTCCGCTCCGAGACTCTGCTGCCAA 905
316 ATGACCTGTCTGAACCCAGCTGCGCCAGACACTCCCTCTGCTGATTCCTGCTGTCAG 375
906 GCCTGCAAGATGAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 965
376 ACTGCAAGACAGGACCACTGAGAGTTCACAGAGAGAAACTTGACACAGCTGCAGCAT 435
966 GGGGTGAGACATCTCAGGATCCATGTTTCCAGTGTGAGGAGAAAGAGAGGCCCGGGC 1025
436 GGAGAGAGACATTCAGGATCCATGCTC-----GGAGAGAGAGAGGCCCGCAGC 483
1026 ACCCAGCCCTCAGCTGAGCTGAGCCCTCTGAGCTTCATCTCTGCTCCCTGCTCAGACCC 1085
484 ACGCCAGACCCAGCAGCTCAGCTCCCTCTGGGCTTCATCTCTGCTCCCTGCTCAGTCA 543
1086 AAGGAGCAGCAGCAGCAACTGTCAAGATCGTCTGAAGAGAGAAACATGAAGAGCTGT 1145
544 GTAGGAATGGCAGCAGCAACCATCAAGATTATCTTGAAGAGAGAAACATGAAGAGCTTC 603
1146 GTGATGCGGGAAGACGCTACTTCCACAGCG-GGAGGTGTGGCACCCTGCTGCTGCTT 1204
604 ACACAGATGGGACGACATATCTCCATGCGGAGGTGTGGCACCCTGCTGCTGCTGCTA 663
1205 CGGCCCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1264

664 TGGACCAATGGCTGATCTCTGACATGTTATCGATGCTACCAGGACTGGCAACGTGT 723

1265 GACCTGTCCACCGAGTACCCCTGCGG 1291

724 GACCTGGCCACACCAATATCCCTGCAG 750

Db

BE911015 915 bp mRNA linear EST 29-SEP-2000

601662108F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3962352 5',

RNA sequence.

BE911015

BE911015.1 GI:10407999

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1. (bases 1 to 915)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM9128 row: p column: 01

High quality sequence stop: 743.

Location/Qualifiers

1. .915

/organism="Mus musculus"

/mol_type="mRNA"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:3962352"

/tissue_type="tumor, biopsy sample"

/dev_stage="10 months, virgin"

/lab_host="DH10B"

/clone_lib="NCI_CGAP_Mam1"

/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Library constructed by Life Technologies. Investigator

providing samples: Gilbert Smith, NIH"

BASE COUNT 211 a 291 c 226 g 187 t

ORIGIN

Query Match 21.5%; Score 389.8; DB 10; Length 915;

Best Local Similarity 71.4%; Pred. No. 9.9e-92;

Matches 588; Conservative 0; Mismatches 217; Indels 18; Gaps 5;

689 TCCTCTGAGCTCGGCGCCGACCAAGTCTGCCAGCACACGGGACCATGTACCAACA 748

14 TCCTCTGGCTCCGAGTTCCTCCCTAAAGTCTGCCAGCTCAATGAGACACATACCAACA 73

749 CGGAGAGATCTTCAGTGCCCATGAGCTGTCCCTCCGCTGCCCAACCACTGTGTCT 808

74 TGGAGAGATCTTCAGTGCCCGAGGAGTGTTCCTGCGCGCTGTCCCAACCACTGTCT 133

809 CTCAGCTGCACAGAGGGCCAGATCTACTCGGGCTCACAACCTGCCCGGACCAAGGCTG 868

134 GTGTAGCTGTATTGAAGGCCACACATCTACTGTGTCTATGACCTGTCTGACCCAGCTG 193

869 CCCAGCACCCCTCCCGTGCAGACTCTGTGTGCCAAGCTGTGCCAAGATGAGCGAAGTGA 928

194 CCCCACACACTCCCTCTGCTGATTCCTGCTGTGCAGACCTGCCAAGACAGGACCACTGA 253

929 GCAATCGGATGAAGAGGACAGTGTGCAGTGCCTCCATGGGGTGAGACATCCTCAGATCC 988

Db

254 GAGTTCACAGAGAAAACCTTGACACAGCTGCAGCATGGAGAGACATTCCTCCAGGATCC 313

989 ATGTTCCAGTGTCTGGGAGAAAGAGAGAGCCCGGACACCCCGGAGTGTCTCCAGTGCCTCAG 1048

314 ATGCTC-----GGAGAGAGAGAGCCCGGACACCGCCAGCCCGGAGAGATCTCAG 361

1049 CGCCCTCTGAGCTTCATCCCTCGCCACCTTCAGACCCAAAGGGAGAGGAGCAGCAACTGT 1108

362 CTCCTCTCTGGCTTCATCCCTCGCCACTTCAGTCACTAGTAGGAATGGGAGCACAACCAT 421

1109 CAAGATCTCTCTGAAGGAGAAACATAAAGAGCTGTGTCTCATGGCGGGAGAGAGTACTC 1168

422 CAAGATTATCTTGAAGGAGAAACATAAAGAGCTTCACACACAAATGGGAGACATACTC 481

1169 CAAGGGAGAGTGTGGCACCCCGGCTTCGCTGCTTGGGCGCCCTTGGCTGCTATCTCTATG 1228

482 CCATGGGAGAGTGTGGCACCCCGGCTTCGCTGCTTGGGCGCCCTTGGCTGCTATCTCTG 541

1229 CACCTGTGAGGATGGCGGACGAGCTGC-CAGCGTGTGACCTGTCCACCGGAGTACCCCT 1287

542 CACATGTATTGATGGCTACGAGACTGCACCGTGTGACCTGTCCCGCCACCCCAATATTCCT 601

1288 GCGGTCAACCCCGAGAAAGTGGCTGGGAAGTGTCTGCAAGAT-TTCCCGAGAGGACAAAGCA 1346

602 GCAGTCAACCCCGAGAAAGTGGCTGGGAAGTGTCTGCAAGATCTTCCCGAGAGGAGCGG 661

1347 GACCTGGCCACAGTGTGAGTCTTCTACAGTGTCTCCAGGAGGAGGAGGAGGAGTCTC 1406

662 GAAGATGACACAGTGTGAGTCTTCCACCGGAGTGTCCAGGATATCAGG--CAGTTCAG 719

1407 GTCCACACATCGTATCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1466

720 GTGTACCCGCTGCTCTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 777

1467 GCCTGGAGCTGTGTGAGAGTCTACCTCTGGAAGTGTGTAAGG 1509

778 GCCTGTGGCCAGGATGCTGTCTTGGGACATCTGTCGAAAG 820

Db

RESULT 10

AW083466/c

LOCUS

DEFINITION

xc02b12.x1 NCI_CGAP Co21 Homo sapiens cDNA clone IMAGE:2583071 3',

similar to contains_MER22.t1 MER22 repetitive element ;, mRNA

sequence.

AW083466

AW083466.1 GI:6038542

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 391)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life

Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The

I.M.A.G.E. Consortium DNA Sequencing by: Washington University

Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 368.

Location/Qualifiers

1. .391

/organism="Homo sapiens"

source

FEATURES

Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vectors identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCAGTCAGCAGC
Plate: 70 row: D column: 6
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Location/Qualifiers
1. .474
FEATURES
source

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/db_xref="taxon:9913"
/tissue_type="pooled"
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/clone_lib="MARC 3BOV"
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BASE COUNT      137 a    124 c    118 g    95 t
ORIGIN
Query Match          20.9%; Score 379.2; DB 10; Length 474;
Best Local Similarity 89.0%; Pred. No. 4.7e-89;
Matches 422; Conservative 0; Mismatches 48; Indels 4; Gaps 1;

1326 ATTTGCCCCAGAGACAAGCAGACCGCTGGCCCAAGTGAGATCAGTGTTCACCAAGTGTCC 1385
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   1 ATTTGTCCAGAGACAAGGCAGACTCGGCCCAAGTGAGATCAGTGCCCAAGTGTCCG 60

1386 AAGGCACCGGGCGGGTCTCTGCTCCACACATCGGTATCCCAGCCGACACACCTGCGT 1445
   |||||
   61 AAGGCGCCAGGTGAGTCTCTGTTTACACGTAGTATCCCCAAGCCCGGACACCTGCGT 120

1446 CGCTTTGCCCTGGAAACA CAGAGCCCTCGGACTTGGTGGAGATCTACCTCTGGAACTGGTA 1505
   |||||
   121 CGCTTTGCCCTCGAGCGTGAGCCCTCTGAGAGGTGGAGATCTACCTCTGGAACTGGTG 180

1506 AAAGATGAGGAACCTGAGGCTCAGAGAGGTGAAGTACCTGGGCCCAAGGCCACACACCAG 1565
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   181 AAAGATGAGGAACCTGAGGCTCAGAGAGGTGAAGTACCTGGGCCCAAGGCCACACACCAG 240

```

Db	QY	Db	QY	Db	QY	Db	QY	Db	QY
241	ATCTTTCCACTTAATTCAGATCAAGAAAGTCAAGAAAGAACTTCCAGAAAGAGCTCA	300							
1626	GCACCTTCCGACTGCTCGCTGGCGCCGCCACCAAGAGTCACTGGAAAGCTTCTGCTAGCCGAGAC	1685							
301	GAACTTCGGGTGCTCACGGGCACCCACGAAGGTCACTGGAAACATCTTCTAGCCGAGAC	360							
1686	CCTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAGACATAACAAAGA	1741							
361	CCCGAGCTGAAGGTCAAGGCCAGTCCAGACAAATGACCAAGACCTTATAACAAAGATC	420							
1742	CTAACAGTTGCAGATGATGAGCTGTATATAATGTTGTTATTATATATATTAATAATA	1795							
421	TGAACAGTTGCAGATGATGAGCTTATCAATTTTGTGTTATATATATTAATAATA	474							

RESULT 12	AA040433/c	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
	AA040433	421 bp	mRNA	linear	EST 10-MAY-1997			
	zk45c09.sl	Soares_pregnant_uterus_NbHPU	Homo sapiens	cdna	clone			
	IMAGE:485872	3', mRNA	sequence.					
	AA040433							
	AA040433.1	GI:1516711						
	EST.							
	Homo sapiens	(human)						
	Homo sapiens	organs						

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 421)
Hillier L., Lennon G., Becker M., Bonaldo M.F., Chiapelli B., Chissee S., Dietrich N., Dubucue T., Favello A., Gish W., Hawkins M., Hultman M., Kucaba T., Lacy M., Le M., Le N., Mardis E., Moore B., Morris M., Parsons J., Prange C., Rifkin L., Rohlfing T., Schellenberg K., Soares M.B., Tan F., Thierry-Mieg J., Trevasaki E., Underwood K., Wohlmann P., Waterston R., Wilson R. and Warra M., Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
97044478
8889549
COMMENT
Contact: Wilton RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1346 Std Error: 0.00
Seq primer: -40M13 fwd. from Amerisham
High quality sequence stop: 341.
Location/Qualifiers
1. 421
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/db_xref="taxon:9606"
/clone="IMAGE:485872"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Soares_pregnant_uterus_NbHPU"
/note="Organ: uterus; Vector: p77T3-Pac; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', AACTGGAGATTCGGCGCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p77T3 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."
BASE COUNT 81 a 95 c 111 g 130 t 4 others
Query Match 18.7%; Score 340.6; DB 9; Length 421;
Best Local Similarity 96.4%; Pred. No. 7.3e-79;
Matches 370; Conservative 0; Mismatches 10; Indels 4; Gaps 2;
QY 1437 AACCTGCGTCGCTTTGCCCTGGAACAC--GAGGCTCGGACTTGGTGGAGATCTACCTC 1493
DB 393 AACCTNGTCGCTTTGCCCTGGGACACNGAGGCTCGGACTTGGTGGAGATCTACCTC 324
QY 1494 TCGAAGCTGGTAAAGATGAGGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGG 1553
DB 323 TCGAAGCTGGTAAAGATGAGGAACTGAGGCTCAGAGAGGTGAAGTACCTG-CCAAGG 265
QY 1554 CCACACAGCCAGATCTTCCACTTGACTCAGATCAAGAACTCAGGAGCAAGACTTCCA 1613
DB 264 CCACACAGCCAGATCTTCCACTTGACTCAGATCAAGAACTCAGGAGCAAGACTTCCA 205
QY 1614 GAAAGAGGCACACACTTCCGACTGCTCGCTGGGCCCCACGAAAGTCACTGGAAGCTCTT 1673
DB 204 GAAAGAGGCACACACTTCCGACTGCTCGCTGGGCCCCACGAAAGTCACTGGAAGCTCTT 145
QY 1674 CCTAGCCACAGCCCTGAGCTGAAGGTTCAGGCGGAGTCCAGACAAAGTGAACAAGACATA 1733
DB 144 CCTAGCCACAGCCCTGAGCTGAAGGTTCAGGCGGAGTCCAGACAAAGTGAACAAGACATA 85
QY 1734 ACAAGACCTAACAGTTCGAGATGAGAGTGTATAATTGTTGTTATATATATATAATAA 1793

Db 84 ACAAAGACCTAACAGTTGCAGATATGAGCTGTATATATTGTTGTTATATATATAATAA 25
QY 1794 TAGAAGTTGCATTAACCATCAAAA 1817
DB 24 TAAGAAGTTGCATTACCTCAAAA 1
RESULT 13
AI205645/c 329 bp mRNA linear EST 29-NOV-1998
AI205645 LOCUS qg30g03.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1836724
DEFINITION 3', similar to gb:X57025 final INSULIN-LIKE GROWTH FACTOR IA
PRECUSOR (HUMAN); mRNA sequence.
ACCESSION AI205645
VERSION AI205645.1 GI:3764317
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 329)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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Seq primer: -40UP from Gibco
High quality sequence stop: 318.
Location/Qualifiers
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/clone="IMAGE:1836724"
/sex="male"
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/clone_lib="Soares testis NHT"
/note="Vector: p77T3-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5', TGTTCACATCTGAAGTGGAGCGCGCCCAATTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p77T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 63 a 75 c 77 g 114 t
ORIGIN
Query Match 17.7%; Score 320.8; DB 9; Length 329;
Best Local Similarity 99.4%; Pred. No. 1.1e-73;
Matches 322; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1494 TCGAAGCTGGTAAAGATGAGGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGG 1553
DB 329 TCGAAGCTGGTAAAGATGAGGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGG 270
QY 1554 CCACACAGCCAGATCTTCCACTTGACTCAGATCAAGAACTCAGGAGCAAGACTTCCA 1613
DB 269 CCACACAGCCAGATCTTCCACTTGACTCAGATCAAGAACTCAGGAGCAAGACTTCCA 210
QY 1614 GAAAGAGGCACACACTTCCGACTGCTCGCTGGGCCCCACGAAAGTCACTGGAAGCTCTT 1673

b 209 GAAAGAGGACAGCACTCCGAGTCTCGTGGCCCCCACGAAGTCACTGGAACGTCTT 150
Y 1674 CTTAGCCCGAGACCTTGAGTGAAGGTCAAGCCAGTCCAGCAAAAGTGAACAGACATA 1733
b 149 CTTAGCCCGAGACCTTGAGTGAAGGTCAAGCCAGTCCAGCAAAAGTGAACAGACATA 90
Y 1734 ACAAGACCTTAACAGTTCAGATATGAGCTGTATATTTGTTATTATATATTAATAA 1793
b 89 ACAAGACCTTAACAGTTCAGATATGAGCTGTATATTTGTTATTATATATTAATAA 30
Y 1794 TAAGAAGTTGCATAAACCATAA 1817
b 29 TAAGAAGTTGCATTACCTCAAAA 6

RESULT 14
LOCUS BI067140 629 bp mRNA linear EST 15-JUN-2001
DEFINITION pgfin.pk010.n11 normalized chicken fat cdna library gallus
CDNA clone pgfin.pk010.n11 5' similar to gb|AAH02909.1|AAH02909
(BC002909) Similar to chordin-like [Homo sapiens], mRNA sequence.
CCESSION BI067140
ERSION BI067140.1 GI:14474662
EYWORDS EST.
OURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 629)
AUTHORS Cogburn,L.A., Morgan,R.W. and Burnside,J.
TITLE Chicken ESTs from fat
JOURNAL Unpublished
COMMENT Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.

FEATURES
source
1. 629
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="pgfin.pk010.n11"
/sex="Male and Female"
/tissue type="fat"
/lab host="E.coli EMDH10B"
/clone lib="normalized chicken fat cdna library"
/notes="Vector: pSPOR11"
BASE COUNT 142 a 191 c 167 g 120 t 9 others
RIGIN

Query Match 16.5%; Score 300.4; DB 12; Length 629;
Best Local Similarity 69.8; Pred. No. 3.8e-68;
Matches 417; Conservative 0; Mismatches 179; Indels 1; Gaps 1;
Y 639 CTTGTACGAGGACGACAGCAATGCTGCCAAGTGTGTGGAACTTCACACTCCCTCTGGA 698
b 2 CCGGTACAGACCCCGAGCAGTGTGCCACGGTGTCTTGAGCCAAATTCCTCTGTGT 51
Y 699 CTCGGGCCCCACCAAGTCTGTCCAGACACACGAGGACCATGTACCAACAGGAGATC 758
b 62 CTCGGGCACTGTGACGCTGTGCGCAGTACAAATGGGACGACGTACCAAGGAGAGATG 121
Y 759 TTGAGTCCCATGAGCTGTTCCTCCCTCGGCTGCCAACACAGTGTCTCTGCGAGTGC 818
b 122 TTCACCAACCACTGAGCTCTTCCCAAGCGCGCCAGCCCAACCACTGTGTGCGAGTGC 181
Y 819 ACAGAGGGCCAGATCTACTCGGGCTCACAACTGCCCGGACCAAGGCTGCCACACACC 878
b 182 TCTGAAGGCCAGATTTACTGTGGCTTGTGTGACCTGCCAGAGCTGTGTGCTCCAAATCCC 241

QY 879 CTCCCGTCCGACACTCCTGTCTGCAAGCCTGCAAGATGAGCAAGTCCAGCAATCGAT 938
DB 242 CTAACCGTGCAGACTCCTGTCTGCAGGTCTGCAAGATGCTCATATGAGAAGTCTGCG 301
QY 939 GAAGAGCACAGTGTGCACTGCTCATGCGGTGAGACATCCTCAGATCCATGTTCCAGT 998
DB 302 GAAGAGAACCCCTGCTAGTTAAACAGAGGTGTTAGGCACTCACAGACCAAGTCTGGGG 361
QY 999 GATGTGGGAGAAAGAGAGGCCCCGCGCACCCAGCCCCCCTGCGCTCAGCGCCCCCTGTG 1058
DB 362 GAAGCAATGGGAGAGGCGCCACCCGCGGACCCCGGTCCACCATGCTCAGTTCCTCACTG 421
QY 1059 AGCTTATCCTCGCCACTTCAGACCCAGAGGAGC-AGCAGCACAACTGTCAAGATCGT 1117
DB 422 GAGTTTATCCCGAGGAGCTTCAAAACCCCAAGGNNAGGTGGCACCCTGTGAAGATCGT 481
QY 1118 CCTGAAGGAGAAACATAGAAAGCCTGTGTCATGCGCGGAGAGCGTACTCCACCGGGA 1177
DB 482 CTTGAAGAGAGACACAGAAAGCCTGTGTTTCAATGGAGAGCCTACTCCCATCGAGA 541
QY 1178 GGTGTGGCACCCCGCCCTTCGCTGCTTGGCGCCCTTGCCTGCTATCCCTATGACACTG 1234
DB 542 AGTGTGGCACCCCGCTCTTCGGGCTCTATGGGCTCTGCGCTGCTGCTGTCACCTG 598

RESULT 15
LOCUS BI456773 942 bp mRNA linear EST 21-AUG-2001
DEFINITION 603174663F1 NCI_CGAP_Mam5 Mus musculus cdna clone IMAGE:5254095 5',
mRNA sequence.
ACCESSION BI456773
VERSION BI456773.1 GI:15247429
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 942)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-f@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1641 row: n column: 16
High quality sequence start: 2
High quality sequence stop: 833.

FEATURES
source
1. 942
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5254095"
/tissue type="tumor, gross tissue"
/dev stage="7 months"
/lab host="DH10B"
/clone lib="NCI CGAP Mam5"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Salt;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

BASE COUNT 204 a 294 c 226 g 218 t
ORIGIN
Query Match 16.4%; Score 297.4; DB 12; Length 942;

Best Local Similarity 70.3%; Pred. No. 2.8e-67;		Mamm. Genome 13 (8), 475-478 (2002)	
Matches 529; Conservative 0; Mismatches 206; Indels 18; Gaps 9;		22213789	
		12226715	
		Contact: Smith TPL	
		USDA, ARS, US Meat Animal Research Center	
		PO Box 166, Clay Center, NE 68933-0166, USA	
		Tel: 402 762 4366	
		Fax: 402 762 4390	
		Email: smithemail.marc.usda.gov	
		Single pass sequencing. Bases called and trimmed with phred	
		v0.980904.e. Vector identified by cross_match with the -minscore 20	
		and -minmatch 12 options.	
		PCR Primers	
		FORWARD: AGGAAACAGCTATGACCAT	
		BACKWARD: GTTTCACAGTCACGACG	
		Plate: 29 row: I column: 10	
		Seq primer: ATTATAGTCACATATAG.	
FEATURES		Location/Qualifiers	
source		1..352	
		/organism="Sus scrofa"	
		/mol_type="mRNA"	
		/db_xref="taxon:9823"	
		/tissue_type="pooled"	
		/lab_host="DH10B"	
		/clone_lib="MARC 2P1G"	
		/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;	
		Library made from pooled tissue from testis, ovary,	
		endometrium, hypothalamus, pituitary, and placenta."	
BASE COUNT		76 a 116 c 107 g 53 t	
ORIGIN			
Query Match		16.2%; Score 294.6; DB 9; Length 352;	
Best Local Similarity		90.3%; Pred. No. 1e-66;	
Matches 315; Conservative 0; Mismatches 34; Indels 0; Gaps 0;			
QY	1229	CACCTGTGAGGATGGCGGCAGGACTGCCAGCTGACCTGTCCACCGAGTACCCCTG	1288
Db	4	CACGGGTCCGCGCGCGCGCGGAGCTGCCAGCTGACCTGTCCACCGAGTACCCCTG	83
QY	1289	CCGTGACCCCGAGAAAGTGTGGGAGTCTGCAAGATTGCCCAGAGGACAAAGCAGA	1348
Db	64	CCATGCCCCCGAGAAAGTGTGGGAGTCTGCAAGATTGTCAGAGGACAAAGCAGA	123
QY	1349	CCCTGCCCCAGTGAGATCAGTTCTACCAAGTGTCCCAAGGACCGGGCCGGGTCTCTG	1408
Db	124	CCCTGCCCCAGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG	183
QY	1409	CCACATCGTATCCCAAGCCAGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1468
Db	184	CCACATCGTATCCCAAGCCAGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	243
QY	1469	CTCGGACTTGTGGAGATCTACCTCTGGAAGCTGTAAGATGAGGAACTGAGGCTCA	1528
Db	244	CTCGGAGCTGAGTCTACCTCTGGAAGCTGTAAGATGAGGAACTGAGGCTCA	303
QY	1529	GAGAGTGAAGTACCTGGCCCAAGGCCACACAGCAGCAATCTTCCACTT	1577
Db	304	GAGAGTGAAGTACCTGGCCCAAGGCCACACAGCAGCAATCTTCCACTT	352
RESULT 17			
BF134285			
LOCUS		601784261.F1 NC1_CGAP_Iu30 Mus musculus cDNA clone IMAGE:4012143 5',	
DEFINITION		mRNA sequence.	
ACCESSION		BF134285	
VERSION		BF134285.1 GI:10973325	
KEYWORDS		EST.	
SOURCE		Mus musculus (house mouse)	
ORGANISM		Mus musculus	
REFERENCE		Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
		1 (bases 1 to 716)	

Best Local Similarity 70.3%; Pred. No. 2.8e-67;		Mamm. Genome 13 (8), 475-478 (2002)	
Matches 529; Conservative 0; Mismatches 206; Indels 18; Gaps 9;		22213789	
		12226715	
		Contact: Smith TPL	
		USDA, ARS, US Meat Animal Research Center	
		PO Box 166, Clay Center, NE 68933-0166, USA	
		Tel: 402 762 4366	
		Fax: 402 762 4390	
		Email: smithemail.marc.usda.gov	
		Single pass sequencing. Bases called and trimmed with phred	
		v0.980904.e. Vector identified by cross_match with the -minscore 20	
		and -minmatch 12 options.	
		PCR Primers	
		FORWARD: AGGAAACAGCTATGACCAT	
		BACKWARD: GTTTCACAGTCACGACG	
		Plate: 29 row: I column: 10	
		Seq primer: ATTATAGTCACATATAG.	
FEATURES		Location/Qualifiers	
source		1..352	
		/organism="Sus scrofa"	
		/mol_type="mRNA"	
		/db_xref="taxon:9823"	
		/tissue_type="pooled"	
		/lab_host="DH10B"	
		/clone_lib="MARC 2P1G"	
		/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;	
		Library made from pooled tissue from testis, ovary,	
		endometrium, hypothalamus, pituitary, and placenta."	
BASE COUNT		76 a 116 c 107 g 53 t	
ORIGIN			
Query Match		16.2%; Score 294.6; DB 9; Length 352;	
Best Local Similarity		90.3%; Pred. No. 1e-66;	
Matches 315; Conservative 0; Mismatches 34; Indels 0; Gaps 0;			
QY	1229	CACCTGTGAGGATGGCGGCAGGACTGCCAGCTGACCTGTCCACCGAGTACCCCTG	1288
Db	4	CACGGGTCCGCGCGCGCGGAGCTGCCAGCTGACCTGTCCACCGAGTACCCCTG	83
QY	1289	CCGTGACCCCGAGAAAGTGTGGGAGTCTGCAAGATTGCCCAGAGGACAAAGCAGA	1348
Db	64	CCATGCCCCCGAGAAAGTGTGGGAGTCTGCAAGATTGTCAGAGGACAAAGCAGA	123
QY	1349	CCCTGCCCCAGTGAGATCAGTTCTACCAAGTGTCCCAAGGACCGGGCCGGGTCTCTG	1408
Db	124	CCCTGCCCCAGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG	183
QY	1409	CCACATCGTATCCCAAGCCAGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1468
Db	184	CCACATCGTATCCCAAGCCAGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	243
QY	1469	CTCGGACTTGTGGAGATCTACCTCTGGAAGCTGTAAGATGAGGAACTGAGGCTCA	1528
Db	244	CTCGGAGCTGAGTCTACCTCTGGAAGCTGTAAGATGAGGAACTGAGGCTCA	303
QY	1529	GAGAGTGAAGTACCTGGCCCAAGGCCACACAGCAGCAATCTTCCACTT	1577
Db	304	GAGAGTGAAGTACCTGGCCCAAGGCCACACAGCAGCAATCTTCCACTT	352
RESULT 17			
BF134285			
LOCUS		601784261.F1 NC1_CGAP_Iu30 Mus musculus cDNA clone IMAGE:4012143 5',	
DEFINITION		mRNA sequence.	
ACCESSION		BF134285	
VERSION		BF134285.1 GI:10973325	
KEYWORDS		EST.	
SOURCE		Mus musculus (house mouse)	
ORGANISM		Mus musculus	
REFERENCE		Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
		1 (bases 1 to 716)	

NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM9252 row: j column: 16
 High quality sequence stop: 658.
 Location/Qualifiers
 1..716
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CZECH 11"
 /db_xref="taxon:10090"
 /clone="IMAGE:4012143"
 /tissue_type="tumor, metastatic to mammary"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Lu30"
 /notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; transgenic model WNT-1, expression driven by
 MMTV-1TR enhancer; Cloned unidirectionally. Primer: Oligo
 dT. Library constructed by Life Technologies.
 Investigator providing samples: Gilbert Smith, NIH"
 152 a 218 c 181 g 165 t

Query Match	15.8%; Score 287.2; DB 10; Length 716;
Best Local Similarity	76.3%; Pred. No. 1.2e-64;
Matches 380; Conservative	0; Mismatches 113; Indels 5; Gaps 2;
472	GCCACACATGTTCTGCTTTTCCATGGGAAGATATCTCCCGCGGAGAGCTGCGACC 531
188	GCTCGGGCAAAGTCTGCTTTTCGGTGAAGAATATATACCCCGCGCCAGAGCTGCACC 247
532	CTTACTTGGAGCACACAGGCGCTGATGTACTCGCTCGCTGTACTTCTCAGAGGGCGCCC 591
248	CCTACTTGGAAACACACAGGCACGATATACTCGTGCCTGTACTCTCTGAGAAATGGAC 307
592	ATGTGAGTTCTTACCGCTTCCACGTCCCGCTGTCCACTGCCCGCCAGACCTGTGACGAGC 651
308	ATGTGAACCTGTTACCGCTTCGCTGCCACCCCTTCACTGCTCAAGCTGTGATGGAGC 367
652	CACAGCAATGCTGTCCCAAGTGTGGAACTCACACTCCCTCTGAGCTCCGCGGCCCCAC 711
368	CACAGCAATGCTGTCCCAAGTGTGGATCTCATGTGCCCTTCGAGTTCCCC 427
712	CAAAGTCTGCCAGCACAAACGGGACCATGTACCAACAGGAGAGATCTTCAGTGCCCATG 771
428	TAAAGTCTGCCAGCTCAATGAGACCATACCAACATGGAGAGATCTTCAGTGCCCAGG 487
772	AGCTGTTCCCTCCGCTGCCAACCAAGTGTCTCTGTGACGTGCACAGAGGGCCAGA 831
488	AGCTGTTCCCTGCCGCTGTCCAAACAGTGTCTCTGTGAGCTGTATGAAGG--CACA 545
832	TCTACTCGGCGCTCAACACTGCCCGCAACAGGCTGCCAGCACCCCTCCGCTGCCAG 891
546	CTTACTGTGTCTCATGACCTGTCTGAAACCATGTGCCACCAATCCCTC--TGCTG 602
892	ACTCTGCTGCCAAGCTGTCAAAGATGAGGCAAGTGTAGCAATCGGAATGAAGAGGACAGTG 951
603	ATTCTCTGCTGTACACCTGCAAAGACAGGACAACTGTAGAGCTCCACAGAAGAAAATTGA 662
952	TGCAGTTCGCTCCATGGGG 969
663	ACCAGGTGCAGCATGGGG 680

RESULT 18	AW425392	373 bp	mRNA	linear	EST 25-APR-2001
LOCUS	AW425392	572933	MARC 2BOV Bos taurus	CDNA 5', mRNA	sequence.
DEFINITION	AW425392				
ACCESSION	AW425392				
VERSION	AW425392.1	GI:6953339			
KEYWORDS	EST.				
SOURCE	Bos taurus (cow)				
ORGANISM	Bos taurus				
REFERENCE					
AUTHORS	Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrnenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Perteira, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.				
TITLE	Sequence evaluation of four pooled-tissue normalized bovine CDNA libraries and construction of a gene index for cattle				
JOURNAL	Genome Res. 11 (4), 626-630 (2001)				
MEDLINE	21180013				
PUBMED	11282978				
COMMENT	Contact: Smith TPJ USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options. PCR Primers FORWARD: AGGAACACAGCTATGACCAT BACKWARD: GTTTCCTCAGTCACGACG Plate: 28 row: G column: 24 Seq primer: ATTAGTGACACTATAG. Location/Qualifiers 1..373 /organism="Bos taurus" /mol_type="mRNA" /db_xref="taxon:9913" /tissue_type="pooled" /lab_host="DH10B" /clone_lib="MARC 2BOV" /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."				
BASE COUNT	85 a	119 c	108 g	61 t	
ORIGIN					

	Query Match	15.4%;	Score 279.2;	DB 9;	Length 373;
	Best Local Similarity	84.4%;	Pred. No. 1.2e-62;		
	Matches 314;	Conservative 0;	Mismatches 58;	Indels 0;	Gaps 0;
QY	925	GTGACCAATCGCATGCAAGAGGACAGTGTGCAGTCGCTCCATCGGTGTGACACATCTCTCAGG	984		
DB	2	GTGAGAGTCGGCTGTGAGAGGACCAACACATGCACCCAGGGGTGAACATTCCCAGG	61		
QY	985	ATTCATGTTTCCAGTGATGCTGGGAGAAAGAGAGGGCCCGGGCACCCGAGCCGCCCATCTGGGCC	1044		
DB	62	ATCTGTGTTTCAGGGGACACGCGGGAGAAAGAGAGACCTGAGCACCCCGCTCCCCACTTGGGC	121		
QY	1045	TCAGCGCCCTCTGAGCTTTCATCCCTCGGCACCTTCAGACCCCAAGGGAGCAGGCAGCACAA	1104		
DB	122	CAGCGCCCTCTCTGGGCTTCATCCCTCGCCACTTCCGACCAAGAGGCGCAGCAGCACCA	181		
QY	1105	CTGTCAAGATCTCTGAAAGAGAAACATAGAAAGCCCTGTGTGATGCGCGGAGAGCGT	1164		
DB	182	CAGTCAAGATTCTGTGAGGAGAAACATAGAAAGCCCTGTGTGATGTTGGGAGACAT	241		
QY	1165	ACTTCCACGGGAGGTGTGGCACCCCGGCCCTCCGTGCGCTTCGGGCCCTTGGCCCTCGCATCC	1224		

Db	242	ACTCCATGGGAGTGGGACCGCGCTTCGGTCCATCGTATCCCAA--GCCAGACAACC	1383	CCCAGGACCGGCGGGTCTCTGTCACACATCGTATCCCAA--GCCAGACAACC	1440
Qy	1225	TATGCACTGTAGATGCGCGCCAGGACTGCCAGCGTGTGACTGTCCCAACGATACC	1441	TGCGTCGCTTTCCTCCCTGGAAACAGAGCGCTCGCACTTGTGGAGA-TCTACCTCTGGAG	1499
Db	302	TGGCACCTGTTCAGGATGCGCGCCAGGACTGCCAGCGGTGTCTGCCCCCACTCGGTACC	321	TGCGTCGCTTTCCTCCCTGGAAACAGAGCGCTCGCACTTGTGGAGANTCTTACCTCTGGAAA	262
Qy	1285	CCTGCCGTACCC	1500	CTGGTAAAGATGAGGAAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCCAAGGCCACAC	1559
Db	362	CCTGCCATCACCC	261	GTTTGGTGAAG-----	250
RESULT 19	AA042913/c	AA042913	398 bp	368 bp	linear
LOCUS	zk56e08.s1 Soares pregnant uterus_NbHPU Homo sapiens cDNA clone	zk56e08.s1 Soares pregnant uterus_NbHPU Homo sapiens cDNA clone	398 bp	368 bp	linear
DEFINITION	IMAGE:486854 3', mRNA sequence.	IMAGE:486854 3', mRNA sequence.	398 bp	368 bp	linear
ACCESSION	AA042913	AA042913	398 bp	368 bp	linear
VERSION	AA042913.1	AA042913.1	398 bp	368 bp	linear
KEYWORDS	EST.	EST.	398 bp	368 bp	linear
SOURCE	Homo sapiens (human)	Homo sapiens (human)	398 bp	368 bp	linear
ORGANISM	Homo sapiens	Homo sapiens	398 bp	368 bp	linear
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	398 bp	368 bp	linear
AUTHORS	Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chispe, B., Chispe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.	Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chispe, B., Chispe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.	398 bp	368 bp	linear
TITLE	Generation and analysis of 280,000 human expressed sequence tags	Generation and analysis of 280,000 human expressed sequence tags	398 bp	368 bp	linear
JOURNAL	Genome Res. 6 (9), 807-828 (1996)	Genome Res. 6 (9), 807-828 (1996)	398 bp	368 bp	linear
MEDLINE	97044478	97044478	398 bp	368 bp	linear
PUBMED	889549	889549	398 bp	368 bp	linear
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: estewartson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 705 Std Error: 0.00 Seq primer: -40M13 fwd. from Amersham High quality sequence stop: 317.	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: estewartson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 705 Std Error: 0.00 Seq primer: -40M13 fwd. from Amersham High quality sequence stop: 317.	398 bp	368 bp	linear
FEATURES	source	source	398 bp	368 bp	linear
BASE COUNT	83 a 92 c 110 g 111 t 2 others	83 a 92 c 110 g 111 t 2 others	398 bp	368 bp	linear
ORIGIN	Query Match 14.8%; Score 269.6; DB 9; Length 398; Best Local Similarity 83.9%; Pred. No. 4.3e-60; Matches 364; Conservative 0; Mismatches 14; Indels 56; Gaps 3;	Query Match 14.8%; Score 269.6; DB 9; Length 398; Best Local Similarity 83.9%; Pred. No. 4.3e-60; Matches 364; Conservative 0; Mismatches 14; Indels 56; Gaps 3;	398 bp	368 bp	linear
LOCUS	AW356676	AW356676	368 bp	368 bp	linear
DEFINITION	39202 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.	39202 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.	368 bp	368 bp	linear
ACCESSION	AW356676	AW356676	368 bp	368 bp	linear
VERSION	AW356676.1	AW356676.1	368 bp	368 bp	linear
KEYWORDS	EST.	EST.	368 bp	368 bp	linear
SOURCE	Bos taurus (cow)	Bos taurus (cow)	368 bp	368 bp	linear
ORGANISM	Bos taurus	Bos taurus	368 bp	368 bp	linear
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovinae; Bos.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovinae; Bos.	368 bp	368 bp	linear
AUTHORS	Smith, T.P.L., Grose, W.M., Fraking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrrenkrug, S.C., Bennett, G.L., Heaton, M.P., Jaeger, W.W., Rohrer, G.A., Chitko-McKown, C.G., Perlea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.	Smith, T.P.L., Grose, W.M., Fraking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrrenkrug, S.C., Bennett, G.L., Heaton, M.P., Jaeger, W.W., Rohrer, G.A., Chitko-McKown, C.G., Perlea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.	368 bp	368 bp	linear
TITLE	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle	368 bp	368 bp	linear
JOURNAL	Genome Res. 11 (4), 626-630 (2001)	Genome Res. 11 (4), 626-630 (2001)	368 bp	368 bp	linear
MEDLINE	21180013	21180013	368 bp	368 bp	linear
PUBMED	11282978	11282978	368 bp	368 bp	linear
COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options. PCR Primers FORWARD: AGGAACACGCTATGACCAT BACKWARD: GTTTCCTCAGTCACGACG Plate: 15 Row: 1 Column: 3 Seq primer: ATTAGTGACACTATAG. Location/Qualifiers 1..368 /organism="Bos taurus"	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options. PCR Primers FORWARD: AGGAACACGCTATGACCAT BACKWARD: GTTTCCTCAGTCACGACG Plate: 15 Row: 1 Column: 3 Seq primer: ATTAGTGACACTATAG. Location/Qualifiers 1..368 /organism="Bos taurus"	368 bp	368 bp	linear

[illegible]

AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., Dubuque, T., Favallo, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.

TITLE Generation and analysis of 280,000 human expressed sequence tags

JOURNAL Genome Res. 6 (9), 807-828 (1996)

MEDLINE 97044478

PUBMED 8889549

COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1272 Std Error: 0.00

Seq primer: -40M13 fwd. from AmerSham

High quality sequence stop: 225.

FEATURES

source

1..348

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:3758837"

/db_xref="taxon:9606"

/clone="IMAGE:485123"

/sex="female"

/dev_stage="adult"

/lab_host="DH10B"

/note="Organ: uterus; Vector: pT73-pac; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', AACTGGAAGATTCGGCGCCCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."

BASE COUNT 69 a 86 c 87 g 99 t 7 others

Query Match 14.3%; Score 259.4; DB 9; Length 348;

Best Local Similarity 89.1%; Pred. No. 2e-57;

Matches 310; Conservative 0; Mismatches 33; Indels 5; Gaps 3;

QY 1439 CCTGCTGCTTCCCTGGAACACAGAGGCTCGACTTGGTGAGATCTACCTCT---G 1495

DB 348 CTTGCTGCTTCCCTGGAACACAGAGGCTCGACTTGGTGATTTACCTCATGG 289

QY 1496 GAAGCTGGTAAAGATGAGAAAC-TGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGC 1554

DB 288 AAGCNTGGTAAAGATGAGAAACTTGAGGCTCAGGAGAGGTGAAGTACCTGGCAAGGC 229

QY 1555 CACAGAGCCAGATCTTCCACTTGAATCAGATCAAGAAAGTCAGGAGCAGACTT-CCA 1613

DB 228 CACAGAGCCAGATCTTCCACTTGAATCAGATCAAGAAAGTCAGGAGCAGACTTCCA 169

QY 1614 GAAAGAGGCACACACTTCCGACTGCTCGTGGGCCCCACCAAGGTCACTGGAAGCTTT 1673

DB 168 GAAAGAGNACNAGCACTTCCGACTGCTCGTGGGCCCCACCAAGGTCACTGGAAGCTTT 109

QY 1674 CTTAGCCCCAGACCTTGGAGCTGAAGGTTCAGGCCAGTCCAGACAAAGTGACCAAGACATA 1733

DB 108 CTTAGCCCCAGACCTTGGAGCTGAAGGTTCAGGCCAGTCCAGACAAAGTGACCAAGACATA 49

QY 1734 ACAAGACCTTAACAGTTGCGAGATAGAGCTGTATAATTGTTGTTATTA 1781

DB 48 ACAAGACCTTAACAGTTGCGAGATAGAGCTGTATAATTGTTGTTATTA 1

RESULT 23

AI343625/c

LOCUS AI343625.1

DEFINITION gp11b04.x1 NCI_CGAP_Kids Homo sapiens cDNA clone IMAGE:1917679 3', mRNA sequence.

ACCESSION AI343625

VERSION AI343625.1 GI:4080831

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 347)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco.

FEATURES

Location/Qualifiers

1..347

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1917679"

/tissue_type="2 pooled tumors (clear cell type)"

/lab_host="DH10B"

/clone_lib="NCI_CGAP_Kids"

/note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', AACTGGAAGATTCGGCGCCCAATTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 62 a 87 c 78 g 120 t

ORIGIN

Query Match 13.8%; Score 251.2; DB 9; Length 347;

Best Local Similarity 93.6%; Pred. No. 3e-55;

Matches 262; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1538 AGTACCTGGCCCAAGGCCACAGCCAGATCTTCCACTTGAATCAAGAAAGTCA 1597

DB 280 AGGACGCTCAGGGAAGGGAATGACAGGGAATCTTCCACTTGAATCAAGAAAGTCA 221

QY 1598 GGAGCAAGACTTCCAGAAAGAGGCACAGACTTCCGACTGCTCGTGGCCCCCAGGAG 1657

DB 220 GGAGCAAGACTTCCAGAAAGAGGCACAGACTTCCGACTGCTCGTGGCCCCCAGGAG 161

QY 1658 GTCACCTGGAAGCTTCTTCAGCCAGACCCCTGGAGCTGAAGGTCAAGGCTCCAGACA 1717

DB 160 GTCACCTGGAAGCTTCTTCCTAGCCAGACCCCTGGAGCTGAAGGTCAAGGCTCCAGACA 101

QY 1718 AAGTGACCAAGACATACAAAGACCTTAACAGTTGAGATGAGCTGTATATTGTTT 1777

DB 100 AAGTGACCAAGACATACAAAGACCTTAACAGTTGAGATGAGCTGTATATTGTTT 41

QY 1778 ATTATATATTAATAATAAGAGTTGCATACCATCAAAA 1817

DB 40 ATTATATATTAATAATAAGAGTTGCATACCATCAAAA 1

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RESULT 24
LOCUS AV661482 376 bp mRNA linear EST 16-JAN-2002
DEFINITION AV661482 GLC Homo sapiens cDNA clone GLC8SH06 3', mRNA sequence.
ACCESSION AV661482
VERSION AV661482.1 GI:9882496
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 376)
AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z. and Han,Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE 21625106
PUBMED 11752456
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
source
1..376
Location/Qualifiers
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GLC8SH06"
/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GLC"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 127 a 87 C 96 G 66 T
ORIGIN
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Best Local Similarity 93.6%; Pred. No. 3.1e-55;
Matches 262; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
1538 AGTACCTGGCCCAAGGCCACACAGCCAGATCTTCCACTTGACTCAGATCAAGAAGTCA 1597
56 AGGACGTCAGGAGAGGGGAATGACAGGGAATCTTCCACTTGACTCAGATCAAGAAGTCA 115
1598 GGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGTGGCCCCACGAAG 1657
116 GGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGTGGCCCCACGAAG 175
1658 GTCACTGGAAGCTTCTTACGCCAGACCCCTGGAGCTGAAGTCAAGCCAGTCCAGACA 1717
176 GTCACTGGAAGCTTCTTACGCCAGACCCCTGGAGCTGAAGTCAAGCCAGTCCAGACA 235
1718 AAGTGACCAAGACATAACAAGACCTTAACAGTTGAGATATAGCTGTATATTTGTTT 1777
236 AAGTGACCAAGACATAACAAGACCTTAACAGTTGAGATATAGCTGTATATTTGTTT 295
1778 ATTATATATTATTAATAAAGAGTTGCATACCATCAAAA 1817
296 ATTATATATTATTAATAAAGAGTTGCATACCATCAAAA 335
RESULT 25
LOCUS BE629331 452 bp mRNA linear EST 25-AUG-2000
DEFINITION BE629331 y1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone
IMAGE:3374061 5' Similar to TR:057465 OS7465 CHORDIN. ;, mRNA
sequence.
ACCESSION BE629331
VERSION BE629331.1 GI:9912019
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 452)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rcapbe@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:1083665
Seq primer: -40RP from Gibco.
FEATURES
source
1..452
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:3374061"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
/clone_lib="Soares mammary gland_NMLMG"
/notes="Vector: p7T73D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified p7T73 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 113 a 153 C 101 G 85 T
ORIGIN
Query Match 13.8%; Score 250.8; DB 10; Length 452;
Best Local Similarity 73.3%; Pred. No. 4.3e-55;
Matches 340; Conservative 0; Mismatches 112; Indels 12; Gaps 1;
825 GGCCAGATCTACTCGGCTCACAACCTGCCCGAACCCAGGCTGCCAGACCCCTCCCG 884
61 GGCCACACTTACTGTGTTCTCATGACCTGTCTGAACCCAGCTGCCCCACCACTCCCT 60
885 CTGCCAGACTCTCTGCTCCAAAGCTGCAAGATGAGGCAAGTGAGCAATCGGATGAAG 944
61 CTGCTGATTCTCTGTCTGACACCTGCAAGACAGGCAACCTGAGAGTTCCACAGAAG 120
945 GACAGTGTGAGTCTCTCATGTTGGGTGAGATCTCTGAGTCCATGTTCCAGTGATCT 1004
121 AACTTGACACAGCTGACAGTGGAGAGAGATCTCCAGAGTCCATGCTC----- 170
1005 GGGAGAAAGAGAGCCCGGGCACCCAGCCCTCTGAGCTCAGCGCCCTCTGAGCTTC 1064
171 --GGAGAGGAGAGCCCGGAGCAGCCAGCCAGCCCGCCAGCTCAGCTCCCTCTGGGCTTC 228
1065 ATCCCTCGCCACTTTCAGACCCCAAGGAGCAGCAGCAACCTGTCTAAGATGCTCTGAAG 1124
229 ATCCCTCGCCACTTTCAGTCAAGTAGAATGGGAGCAACCATCAAGATTAATCTTGAAG 288
1125 GAGAAACATAGAAGAGCTGTGTGATGGGGAGAGAGCTACTCCACGGGAGGTGTGG 1184
289 GAGAAACATAGAAAGCTTGCACACAAATGGGAGAGACATCTCCATGGGAGGTGTGG 348
1185 CACCCGGCTTCCGTGCTTGGCCCTTGGCCCTGCTCATCTGACCTGTGAGGATGGC 1244

```

Db 349 CACCCACATGCTCTCTCTTGGCCCCCATGCTCTGTCATCTGTCACATGTCATGCGTGC 408
QY 1245 CCCCAGGACTGCAGGCTGTGACTGTCCACAGGATACCCCTG 1288
Db 409 TACCAGGACTGCACCGTGTGACTGTCCACCAATATCCCTG 452

RESULT 26
CB047807/c
LOCUS
DEFINITION NISC_GJ01b02.xl NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3270458
3', mRNA sequence.
ACCESSION CB047807
VERSION CB047807.1 GI:27786094
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 294)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
CDNA Library Preparation: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
Plate: LLAM8006 row: C column: 3
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers
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/clone="IMAGE:3270458"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pr28"
/notes="Organ: prostate; Vector: p773D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonoids
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 57 a 59 c 70 g 108 t
ORIGIN

Query Match 13.7%; Score 249.8; DB 14; Length 294;
Best Local Similarity 99.2%; Pred. No. 6.6e-55; Indels 0; Gaps 0;
Matches 251; Conservative 0; Mismatches 2;

QY 1565 GAATCTCCACTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCAC 1624
Db 277 GAATCTCCACTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCAC 218
QY 1625 AGCACTTCCGACTGCTCGTGGCCCCCAGAAAGTCACTGGAACTCTTCTTAGCCGAGA 1684
Db 217 AGCACTTCCGACTGCTCGTGGCCCCCAGAAAGTCACTGGAACTCTTCTTAGCCGAGA 158
QY 1685 CCCTGGAGCTGAAGTCAAGGCTCAGCAAAAGTCAAGCAAGTCAAGCAAGTCAAGCAAGTCA 1744
Db 157 CCCTGGAGCTGAAGTCAAGGCTCAGCAAAAGTCAAGCAAGTCAAGCAAGTCAAGCAAGTCA 98

QY 1745 ACAGTTGCAGATGAGCTGTATATTTGTTTATTATATATATATATATATATATATATATATAT 1804
Db 97 ACAGTTGCAGATGAGCTGTATATTTGTTTATTATATATATATATATATATATATATATATAT 38
QY 1805 ATAACCATCAAAA 1817
Db 37 AITACCTCAAAA 25

RESULT 27
CB047808
LOCUS
DEFINITION NISC_GJ01b02.yl NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3270458
5', mRNA sequence.
ACCESSION CB047808
VERSION CB047808.1 GI:27786095
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 294)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
CDNA Library Preparation: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
Plate: LLAM8006 row: C column: 3
Seq primer: M13RPI reverse primer (ABI).
Location/Qualifiers
1. .294
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3270458"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pr28"
/notes="Organ: prostate; Vector: p773D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonoids
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 107 a 70 c 59 g 57 t
ORIGIN

Query Match 13.7%; Score 249.8; DB 14; Length 294;
Best Local Similarity 99.2%; Pred. No. 6.6e-55; Indels 0; Gaps 0;
Matches 251; Conservative 0; Mismatches 2;

QY 1565 GAATCTCCACTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCAC 1624
Db 18 GAATCTCCACTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCAC 77
QY 1625 AGCACTTCCGACTGCTCGTGGCCCCCAGAAAGTCACTGGAACTCTTCTTAGCCGAGA 1684
Db 78 AGCACTTCCGACTGCTCGTGGCCCCCAGAAAGTCACTGGAACTCTTCTTAGCCGAGA 137
QY 1685 CCCTGGAGCTGAAGTCAAGGCTCAGCAAAAGTCAAGCAAGTCAAGCAAGTCAAGCAAGTCA 1744

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138 CCCTGGAGCTGAAGGTACAGGTCAGGCCAGCTCCAGACAAAGTGACCAAGACATACAAAGACCTTA 197
1745 ACAGTTCAGATGAGCTGTATTAATTTGTTATATATATATATATATATATATATATATATATATAT 1804
198 ACAGTTCAGATGAGCTGTATTAATTTGTTATATATATATATATATATATATATATATATATATAT 257
1805 ATACCATCAAAA 1817
258 ATTACCTCAAAA 270

RESULT 28
BF437134/c
LOCUS
DEFINITION
7p63f11.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:3650469 3',
similar to TR:Q9UG17 Q9UG17 HYPOTHETICAL 21.1 KD PROTEIN ;, mRNA
sequence.
ACCESSION
BF437134
VERSION
BF437134.1 GI:1149466
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 228)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -400P from Gibco.
Location/Qualifiers
1..228
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3650469"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI-CGAP_Pr28"
/notes="Organ: prostate; Vector: pVT73D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI CGAP Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonoids
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 47 a 49 c 55 g 77 t
ORIGIN
Query Match 12.4%; Score 224.8; DB 10; Length 228;
Best Local Similarity 99.1%; Pred. No. 2.4e-48;
Matches 226; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1590 GAAAGTCAGGAAGCAAGACTTCCGAAAGAGGACAGACACTTCCGACTCTCGTGGCCCC 1649
228 GAAAGTCAGGAAGCAAGACTTCCGAAAGAGGACAGACACTTCCGACTCTCGTGGCCCC 169
1650 CCACGAAGGTCACTGGAAACGCTTCTCTAGCCAGACCCCTGGAGCTGAAGGTCAAGGCCAG 1709
168 CCACGAAGGTCACTGGAAACGCTTCTCTAGCCAGACCCCTGGAGCTGAAGGTCAAGGCCAG 109
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QY 1710 TCCAGACAAAGTGACCAAGACATACAAAGACCTAACAGTTGCAGATATAGAGCTGTATAA 1769
DB 108 TCCAGACAAAGTGACCAAGACATACAAAGACCTAACAGTTGCAGATATAGAGCTGTATAA 49
QY 1770 TTGTGTTATTATATATTAATAAATAAGAGGTGCTATACCATCAAAA 1817
DB 48 TTGTGTTATTATATATTAATAAATAAGAGGTGCTATACCATCAAAA 1

RESULT 29
BF437637/c
LOCUS
DEFINITION
7p78d05.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:3651896 3',
similar to TR:Q9UG17 Q9UG17 HYPOTHETICAL 21.1 KD PROTEIN ;, mRNA
sequence.
ACCESSION
BF437637
VERSION
BF437637.1 GI:11450052
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 228)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -400P from Gibco.
Location/Qualifiers
1..228
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3651896"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI-CGAP_Pr28"
/notes="Organ: prostate; Vector: pVT73D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI CGAP Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonoids
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 47 a 50 c 55 g 76 t
ORIGIN
Query Match 12.3%; Score 223.2; DB 10; Length 228;
Best Local Similarity 98.7%; Pred. No. 6.4e-48;
Matches 225; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1590 GAAAGTCAGGAAGCAAGACTTCCGAAAGAGGACAGACACTTCCGACTCTCGTGGCCCC 1649
228 GAAAGTCAGGAAGCAAGACTTCCGAAAGAGGACAGACACTTCCGACTCTCGTGGCCCC 169
1650 CCACGAAGGTCACTGGAAACGCTTCTCTAGCCAGACCCCTGGAGCTGAAGGTCAAGGCCAG 1709
168 CCACGAAGGTCACTGGAAACGCTTCTCTAGCCAGACCCCTGGAGCTGAAGGTCAAGGCCAG 109
```

FEATURES

source

2Y 1710 TCCAGACAAAGTGCCAGACATACACAGAGCTACAGCTTGCGATATGAGCTGTATAA 1769
Db 108 TCCAGACAAAGTGCCAGACATACACAGAGCTACAGCTTGCGATATGAGCTGTATAA 49
2Y 1770 TTGTTGTTATTATATATTAATAAATAAGAGTTGCTATACCAACCAAAA 1817
Db 48 TTGTTGTTATTATATATTAATAAATAAGAGTTGCTATACCAACCAAAA 1
RESULT 30
BE629653/c 442 bp mRNA linear EST 25-AUG-2000
LOCUS u36f11.x1 Soares mammary_gland_NMLMG Mus musculus cDNA clone
DEFINITION IMAGE:3374061 3', mRNA sequence.
ACCESSION BE629653
VERSION BE629653.1 GI:9912270
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 442)
JOURNAL NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Other ESTs: uu36f11.v1
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:1083665
High quality sequence stop: 433.
Location/Qualifiers
1..442
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:3374061"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
/clone_lib="Soares mammary gland NMLMG"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - Cligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT73 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 96 a 108 c 109 g 129 t
ORIGIN
Query Match 12.8%; Score 220.8; DB 10; Length 442;
Best Local Similarity 71.8%; Pred. No. 3.7e-47;
Matches 346; Conservative 0; Mismatches 77; Indels 59; Gaps 2;
Y 1320 TGCAGATTGCCCAGAGACAAAGACAGCCCTGGCCACAGTCAGATCAGTTCTACACAGG 1379
Db 442 TGCAGATTGCCCAGAGACAGGAGGAGATGACACAGTGAGTCAITTCACCCGG 383
Y 1380 TGTCCCAAGCCACCGGCGGGCTCTGTCCACATCGGTATCCCAAGCCAGACAC 1439
Db 382 TGTCCCAAGGTACACGCGCAGTTCCAGGTGTACAGTTGGCATCTCAAGCCAGACAGC 323
Y 1440 CTGCGTGGCTTCCCTGGACACAGAGCCCTCGACTTGGTGGAGTCTACTCTGGAG 1499
Db 322 CTACACCGCTTCTCTGGAGCATGAAGCCCTCTGACCAGGTAGAGATGTACATTGGAAG 263
Y 1500 CTGGTAAAGATCAGGAACCTAGGCTCAGAGAGGTGAGTACCTGGCCCAAGCCACAC 1559
Db 262 CTGGTGAAG----- 253

QY 1560 AGCCAGAACTTCCACTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGA 1619
Db 252 -----GAATCTACCACTTGGTTTCAGATCAAGAGAGTCAGGAAGCAAGATTTCAGAAAGA 198
QY 1620 GGCACAGCACTTCCGACTGCTCGCTGGCCCCCAGCAAGAGTCACTGGAAAGCTCTTCCTAGC 1679
Db 197 GGCTCAGAACTTCCGCTGCTCACCAGCCACCCATGAAGGTTACTGGACCGTCTTCCTAGC 138
QY 1680 CCAGACCTGGAGCTGAAGGTCAAGCCAGTCCAGCAAAAGTCCAGCAAGACATCAAAAG 1739
Db 137 CCAGACTCCAGAGCTGAAAGTTACAGCCAGCCAGCAAAAGTCCAGCAAGACATTAAGCA 78
QY 1740 A-----CCTAACAGTTGCAGATATGAGCTGTATATTTGTTGTTATATATATATAATA 1795
Db 77 AGGACCTAAAGAGTTGCAGATACAGAGTTTATTTGGTTTGTATTATATATAATAAGA 18
QY 1796 AG 1797
Db 17 AG 16
RESULT 31
BI286468/c 450 bp mRNA linear EST 19-JUL-2001
LOCUS BI286468
DEFINITION UI-R-DE0-cal-d-09-0-UI.s1 UI-R-DE0 Rattus norvegicus cDNA clone
ACCESSION UI-R-DE0-cal-d-09-0-UI 3', mRNA sequence.
VERSION BI286468
KEYWORDS BI286468.1 GI:14941145
SOURCE EST.
ORGANISM Rattus norvegicus (Norway rat)
REFERENCE Rattus norvegicus
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
JOURNAL Rattus.
MEDLINE 1 (bases 1 to 450)
PUBMED Bonaldo,M.P., Lennon,G. and Soares,M.B.
COMMENT Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
9704477
8889548
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRP, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
The sequence contained an oligo-dt track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dt track served to verify it as a clone from the
non-normalized cervix library cDNA Library Preparation: M.B. Soares
Lab Clone distribution: clones will be available through Research
Genetics (www.resgen.com) The following repetitive elements were
found in this cDNA sequence: 39-60, >Al_rich#Low_complexity
Seq primer: M13 Forward
POLYA=Yes.
Location/Qualifiers
1..450
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-DE0-cal-d-09-0-UI"
/dev_stage="ADULT"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-DE0"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-DE0
library is a non-normalized library constructed from rat

cervix tissue. For a detailed description of the library from which this clone was derived, please visit our web site at ratestat.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)

TAG_LIB=UI-X-DE0
TAG_TISSUE=cervix
TAG_SEQ=GACCA"

SOURCE	ORGANISM	Mus musculus (house mouse)
REFERENCE		1 (bases 1 to 770)
AUTHORS		NIH-MGC http://mgc.nci.nih.gov/ .
TITLE		National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT		Unpublished Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLM9312 row: n column: 03 High quality sequence stop: 752. Location/Qualifiers 1..770 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="IMAGE:4036802" /tissue_type="tumor, gross tissue" /dev_stage="7 months" /lab_host="DH10B" /clone_lib="NCI_CGAP_Man5" /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"
BASE COUNT	228 a	209 c 184 g 149 t
ORIGIN		
Query Match	10.7%	Score 194; DB 10; Length 770;
Best Local Similarity	69.3%	Pred. No. 5.8e-40;
Matches 338; Conservative	0; Mismatches 90; Indels 60; Gaps 3;	
QY	1334	AGAGCAAAAGCAGACCTCGGCCACAGTGGAGATCAGTTCTACCAAGTGTCCCAAGCACC 1393
Db	316	AGAGCAGCAGGCGGAAGATGACCACAGTGAAGTCTCCACCCGGTGTCCCAAGGTACC 375
QY	1394	GGCGGGTCTCTGTCACACATCGGTATCCCAAGCCAGACACCTCGTTCGTTTGC 1453
Db	376	AGCCAGTTTCCAGGTGTACACGTGGCATCTCCAAAGCCAGACACCTACACCGCTTTGT 435
QY	1454	CCTGGAACACGAGCGCTCGGACCTGGTGGAGATCTACCTCTGGAAGCTGGTAAAGATGA 1513
Db	436	CTGGAGCATGAAGCCCTCTGACCAAGTAGAGATGTACATTGGAAGTGGTGAAG--- 491
QY	1514	GGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCAGAATCTTCC 1573
Db	492	-----GAATCTACC 500
QY	1574	ACTTGACTCAGATCAAGAAAGTCAAGGAAGCAAGACTTCAGAAAGAGGCACACACTTCC 1633
Db	501	ACTTGGTTTCAGATCAAGAGAGTCAAGAGCAAGATTTCAGAAAGAGGGTCAGAACTTCC 560
QY	1634	GACTGCTCGTGGCCCCCAGGAAGTCACTGGAAGCTCTTCTAGCCAGACCTCGAGC 1693
Db	561	GGCTGCTCACGGCACCATGAAGGTTACTGGACCGTCTTCTAGCCAGACTTCAGAGC 620
QY	1694	TGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAGACATTAAGCAAGGCTTAAGAGT 1749
Db	621	TGAAGGTTACAGCCAGCCAGACAAAGTGACCAAGACATTAAGCAAGGCTTAAGAGT 680
QY	1750	TCAGATATGAGCTGTATAATTGTTGTTATATATATTAATATAAATAAGAGTTGCATAC 1809
Db	681	TGCAGATACAGATTATATGTTT--TCGCTATTATATATTAATTAATTAATTAATTAATTA 739

2Y 604 ACCGCTCAGTCTCCGCTGTCCACTGCCCGCCAGCGCTGTGACGAGCCACACGAGATGC 662
|||||
Db 467 ACCGCTCAGTCTCCGCTGTCCACTGCCCGCCAGCGCTGTGACGAGCCACACGAGATGC 525
|||||

RESULT 35
AA040432 248 bp mRNA linear EST 10-MAY-1997
LOCUS 2x46c09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
DEFINITION IMAGE:485872 5' similar to contains element PTR5 repetitive element
; mRNA sequence.

ACCESSION
AA040432 GI:1516710
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 248)
REFERENCE
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins
M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moore
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,
Underwood, K., Woldmann, P., Waterston, R., Wilson, R. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)

JOURNAL
MEDLINE 97044478
PUBMED 889549
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1346 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 239.

FEATURES
Location/Qualifiers
1..248
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3759586"
/db_xref="taxon:9606"
/clone="IMAGE:485872"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Soares_pregnant_uterus_NbHPU"
/note="Organ: uterus; Vector: p7T3-Pac; Site: 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5'
AAGTGGAGATTCGCGCGCTTTTCTTTTCTTTTCTTTT 3'].
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p7T3 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."

BASE COUNT 49 a 84 C 52 G 46 T 7 others
ORIGIN

Query Match 10.5%; Score 190.6; DB 9; Length 248;
Best Local Similarity 95.0%; Pred. No. 2.8e-39;
Matches 207; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

2Y 638 GCCTGTGACGAGCCACAGCAATGTGTCTCCAGTGTGTGGACCTCACACTCCCTCTGG 697
31 GCAGGTAGTAGGCGACAGCAATGTGTCTCCAGTGTGTGGACCTCACACTCCCTCTTT 90

2Y 698 ACTCGGGCCCCACCAAGTCTCGCAGCACCGGACCATGTACCAACCGAGAT 757
|||||

Db 91 ACTCGGGCCCCACCAAGTCTCGCAGCACACGAGGACCATGTACCAACACGAGAGAT 150
758 CTTAGTGTCCCAATGAGCTGTTCCTCCCTCCC-GCCTGCCCAACCAAGTGTGTCTCTGCAGCT 816
151 CTTCACTGCCCATGAGCTGTTCCTCCCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCT 210

QY 817 GCACAGAGGGCCAGACTACTCTGCGGCTCACACCTGC 854
211 GCACAGAGGGCCAGACTACTCTGCGGCTCACACCTGC 248

RESULT 36
AA514464 472 bp mRNA linear EST 18-AUG-1997
LOCUS nf57f02.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:924027 3',
DEFINITION mRNA sequence.

ACCESSION
AA514464
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 472)
REFERENCE
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 778 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 472.

FEATURES
Location/Qualifiers
1..472
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:924027"
/sex="pooled"
/tissue_type="colon"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Co3"
/note="Vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; Site: 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from 12 pooled bulk tumor samples and primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified p7T3 vector. Library went through one round of
normalization."

BASE COUNT 97 a 145 c 127 g 103 t
ORIGIN

Query Match 10.0%; Score 181.6; DB 9; Length 472;
Best Local Similarity 97.9%; Pred. No. 8.9e-37;
Matches 184; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1327 TTTCGCCAGAGACAAAGCAGACCTGCCACAGTACAGTACCTTCTTACCAAGTGTCCCA 1386
47 TCTCTCCAGAGACAAAGCAGACCTGCCACAGTACAGTACCTTCTTACCAAGTGTCCCA 106

QY 1387 AGGCACCGGGCGGGTCTCTCGTCCACATCGGTATCCCCAAGCCAGACCACTGGGTC 1446
107 AGGCACCGGGCGGGTCTCTCGTCCACATCGGTATCCCCAAGCCAGACCACTGGGTC 166

QY	1447	GCTTTGCCCTGGAACACAGGAGGCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAA	1506
Db	167	GCTTTGCCCTGGAACACAGGAGGCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAA	226
QY	1507	AAGATGAG 1514	
Db	227	AAGGTGAG 234	
RESULT 37			
AA042926			
LOCUS			
DEFINITION	275 bp mRNA linear EST 10-MAY-1997		
ACCESSION	ZK56E08.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone		
VERSION	AA042926		
KEYWORDS	EST.		
SOURCE	AA042926.1 GI:1522544		
ORGANISM	Homo sapiens (human)		
REFERENCE			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 275)		
TITLE	Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags		
JOURNAL	Genome Res. 6 (9), 807-828 (1996)		
MEDLINE	97044478		
PUBMED	8889549		
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: estewatson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 705 Std Error: 0.00 Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 176.		
FEATURES			
source	1. 275 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="GDB:3760568" /db_xref="taxon:9606" /clone="IMAGE:486854" /sex="female" /dev_stage="adult" /lab_host="DH10B" /clone_lib="Soares_pregnant_uterus_NbHPU" /notes="Organ: uterus; Vector: pT7T3-Pac; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5, AACTGGAAGAAATTCGGCGCCGCTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."		
BASE COUNT	60 a 81 c 75 g 50 t		
ORIGIN			
Query Match	9.8%; Score 177.6; DB 9; Length 275;		
Best Local Similarity	88.8%; Pred. No. 8.1e-36;		
Matches 245; Conservative	0; Mismatches 22; Indels 9; Gaps 5;		
QY	1102	CAACTGTCAAGATCGTCTCGAAGAGAAACATANGAAAGCCTGTGTGCATGCGCGGAAGA	1161

Db	126	CTCAGACACATATTTCGCTGTTTCAAGACAAGAGTATAGAGTGGGTGAGAATGGCATCC	185
QY	533	CTACTTGGAGGCCAACAAGCCCTGATGTACTGCGCTGCGCTGTACCTGCTCAGAGGGCGCCCA	592
Db	186	CTACTTGGAAACCGTATGGAAGTGTGTTTACGTGTGAACCTGCATCTGCTCTGAGAATGGGA	245
QY	593	TGTGAGTTGTTACCGCTTCCACTGTCGCGCTGTCCACTGCCCCCAGCGCTGTGACGAGCC	652
Db	246	TGTGCTTTGACGCCGAGTCAGATGTCCTTCAATGCTTTCACCGTGCATATTCC	305
QY	653	ACAGCAATGCTGTCCCAAGTGTGTGAACCTCACACTCCCTCTGGAATCCCGGCCCCCACC	712
Db	306	TCATCTCTGTTGCCCGCTGCCAGACTCCTTACCACCAAGTGAAACAATAAGGTGACCAG	365
QY	713	AAAGTCTCCGACACACAGCGGACCATGTACCAACACGGAGAGATCTTCACTGCCCATGA	772
Db	366	CAAGTCATGCGAATACAAATGGAACCACTTACCACCATGGAAGACTGTTCATAGCTGAAGG	425
QY	773	GCTGTTCCCTCCCGCTGCCAACACAGGTGTCTCTCTGAGCTGCACAGAGGGCCAGAT	832
Db	426	GCTCTTTAGAACCGGCAACCCAACTCAGTGCAGTCTAGTCTCTCGGAGGGGAATGT	485
QY	833	CTACTGGCGCTCAACACTGCCCCGAAACGAGCTGCCAGCACCCCTCCCGCTGCCAGA	892
Db	486	ATACTGTGTTCAAGACTTGCCCCAACTGACCTGTGCATTCACAGTCTCTGTTCCAGA	545
QY	893	CTCCTGCTGCCAAGCCTCAAGATGAGCAAGTGAAGCAATCGATCAAGAGGACAGTGT	952
Db	546	TTCTTGTGCGGAGTATCGAGAGGGATCGAGAATTATCGTGGAAACATCGGATGGTGA	605
QY	953	GCAGTCGCTCCA-----TGGGTGTGAGACATCTCTCAGGATCCATGTTTCCAGTGA	1000
Db	606	TATCTTCGGCAACCTGCGCAACAGAGAAGCAAGACATTTTACCTCGCTTCCCGCTACGA	665
QY	1001	TGCTGGAGAAAGAGAGCCCGGCGCACCCAGCCCCCATCTGGCTCAGCGGCCCTCTGAG	1060
Db	666	TCCTCCACCAAGCAGACAAGCTGGAGGTCTTCCCGCTTTCTCTGGAGCAGAACTCAACG	725
QY	1061	CTTCATCCCTCGCCACTTCAGACCCCAAGGGAGCAGCAGACACAACCTGTCAAGATCGTCT	1120
Db	726	GGGAGCTGTTATAGATTCCTCAGCAAGCATCCGGGACCATCGTGAGATTTGATCAATAA	785
QY	1121	GAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGGAAGACGTAACCTCCACGGGGAGGT	1180
Db	786	CAAGCAACAACATGGACAGTGTGTGTTTCCCATGGAAACCTACTCTCATGAGAGTTC	845
QY	1181	GTGCAACCCCGCTTCCGTGCTTCCCGCCCTTGGCCCTGCATCTATGCACCTGTGAG	1239
Db	846	CTGSCACCCCAATCTACAGGCAATTGGCATTGTGGAATGTGTACTATGCACCTTGAATG	904
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BE799088			
LOCUS	601584848F1	NIH_MGC_7 Homo sapiens	855 bp linear EST 20-SEP-2000
DEFINITION			CDNA clone IMAGE:3942645 5', mRNA sequence.
ACCESSION			BE799088
VERSION			BE799088.1
KEYWORDS			EST.
SOURCE			Homo sapiens (human)
ORGANISM			Homo sapiens
REFERENCE			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS			1 (bases 1 to 855)
TITLE			NIH-MGC http://mgc.nci.nih.gov/
JOURNAL			National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT			Unpublished
			Contact: Robert Strausberg, Ph.D.
			Email: cgapbs-remail.nih.gov
			Tissue Procurement: DCTP/DTP
			CDNA Library Preparation: Ling Hong/Rubin Laboratory,
			CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCW796 row: j column: 22
High quality sequence stop: 831.

FEATURES

Location/Qualifiers
1. .855
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/notes="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 215 a 207 c 219 g 214 t

ORIGIN
Query Match 8.6%; Score 157; DB 10; Length 855;
Best Local Similarity 58.1%; Pred. No. 3.8e-30;
Matches 277; Conservative 0; Mismatches 200; Indels 0; Gaps 0;

Qy	475	CAGACATGTTCTGCTTTCCATGGGAAGAGATACCTCCCGGGGAGAGCTGGCACCCCT	534
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Qy	535	ACTTGAGCCACAAAGGCTGATGTCCTGCGCTGTACCTGTACCTGTACAGAGGGGCCCATG	594
Db	282	ACCTGGAACCTTATGGGTTGGTTACTGCGTGAATGCATCTGCTCAGAGATGGGAATG	341
Qy	595	TGAGTTGTTACCGCTCCACTGTCGGCTGTCCACTGCCCGCCAGCTGTGACGGAGCCAC	654
Db	342	TGCTTTGACGCCGAGTCAGATGTCCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	401
Qy	655	AGCAATGCTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGGCCCAACAA	714
Db	402	ATCTGTGCTGCCCTGCTGCCAGACTCTTACCCCACTGAGTGAACAAATAGGTGACCA	461
Qy	715	AGTCCTGCCAGCACACGGGACCATGTACCAACACGGAGAGATCTTCACTGCCCATGAC	774
Db	462	AGTCCTGCCAGTACATGCGGACAACTTACCAACATGGAGAGCTGTTCTGTAGCTGAAGGC	521
Qy	775	TGTTCCCTCCCGCTCCCAACCAAGTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	834
Db	522	TCCTTCAGAAATCGGCAACCCCAATCAATGCAACCCAGTCAGCTGTTCCGGAGGAAACGT	581
Qy	835	ACTGGGCTCCACAACTGCCCGCAACCAAGGCTGCCAGACCCCTCCCGCTGCCAGACT	894
Db	582	ATTGTGCTCTCAAGACTTGCCCAAAATTAACCTGTGCTTCCAGTCTCTGTTCAGATT	641
Qy	895	CCTGCTGCCAAGCTGCAAGATGAGGCAAGTGAACAATCGGATGAAGAGCAGTG	951
Db	642	CCTGCTGCCGGTATGACAGAGAGATGAGAACTGTCAATGGGAACATTCTGATGGTG	698

Search completed: January 31, 2004, 03:59:37
Job time : 3973 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 00:30:59 ; Search time 6754 Seconds
(without alignments)
11005.744 Million cell updates/sec

Title: US-09-890-456-8
Perfect score: 1817
Sequence: 1 ggacatacaaaaaggaaaca.....aagttgcataaacatcaaaa 1817

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
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- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1817	100.0	1817	6	AX140202	AX140202 Sequence
2	1772.2	97.5	1890	6	AX140198	AX140198 Sequence
3	1417	78.0	1622	6	AX140203	AX140203 Sequence
4	1344.4	74.0	1722	6	AX140200	AX140200 Sequence
5	1194.4	74.0	1792	6	AX119273	AX119273 Sequence
6	1342.8	73.9	1720	6	AX048199	AX048199 Sequence
7	1342.8	73.9	1732	6	AX092350	AX092350 Sequence
8	1342.8	73.9	1732	6	AX376214	AX376214 Sequence
9	1342.8	73.9	1732	6	AX697073	AX697073 Sequence
10	1338	73.6	1722	6	AX140199	AX140199 Sequence
11	1338	73.6	1722	6	AX140196	AX140196 Sequence
12	1325	72.9	1722	6	AX140204	AX140204 Sequence
13	1297	71.4	1567	6	AX119269	AX119269 Sequence
14	1274.4	70.1	1356	6	AX119269	AX119269 Sequence
15	1256.4	69.1	1281	6	AX140195	AX140195 Sequence
16	1222.8	67.3	1405	6	AX363199	AX363199 Sequence
17	1222.8	67.3	1570	6	AX235836	AX235836 Sequence
18	1143.4	62.9	1290	6	AX119271	AX119271 Sequence
19	1139.2	62.7	1515	6	AX140201	AX140201 Sequence
20	1121.4	61.7	1515	6	AX140197	AX140197 Sequence
21	1026.4	56.5	1517	6	AX363201	AX363201 Sequence
22	750.8	41.3	1516	10	BC019399	BC019399 Mus muscu
23	750	41.3	1829	6	AX235833	AX235833 Sequence
24	732.2	40.3	1428	10	AF38222	AF38222 Mus muscu
25	675.4	37.2	807	6	AX014311	AX014311 Sequence
26	585	32.2	141937	2	AC011686	AC011686 Homo sapi
27	585	32.2	230157	9	AP001324	AP001324 Homo sapi
28	574	31.6	211452	2	AP002010	AP002010 Homo sapi
29	519	28.6	683	9	HSM800814	AL110168 Homo sapi
30	424.8	23.4	1202	6	AX140205	AX140205 Sequence
31	356.2	19.6	422	6	AX014296	AX014296 Sequence
32	340.6	18.7	421	6	AX337465	AX337465 Sequence
33	214.2	11.8	3827	6	AX175123	AX175123 Sequence
34	211	11.6	1864	6	AX175120	AX175120 Sequence
35	211	11.6	3291	10	AF296451	AF296451 Mus muscu
36	209.8	11.5	1803	10	AF321853	AF321853 Mus muscu
37	208.2	11.5	3601	10	BC050818	BC050818 Mus muscu
38	207.8	11.4	2750	10	AF305714	AF305714 Mus muscu
39	204	11.2	2497	9	BC002909	BC002909 Homo sapi
40	199	11.0	1496	6	AX175126	AX175126 Sequence
41	198	10.9	1341	6	AX175130	AX175130 Sequence
42	197	10.8	171006	2	AP002504	AP002504 Homo sapi
43	197	10.8	179727	9	AP001104	AP001104 Homo sapi
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ALIGNMENTS

RESULT 1	AX140202	Sequence 8 from Patent WO0134796.	1817 bp	DNA	linear	PAT 31-MAY-2001
LOCUS	AX140202	Sequence 8 from Patent WO0134796.	1817 bp	DNA	linear	PAT 31-MAY-2001
DEFINITION	AX140202	Sequence 8 from Patent WO0134796.	1817 bp	DNA	linear	PAT 31-MAY-2001
ACCESSION	AX140202	Sequence 8 from Patent WO0134796.	1817 bp	DNA	linear	PAT 31-MAY-2001
VERSION	AX140202.1	GI:14280541	1817 bp	DNA	linear	PAT 31-MAY-2001
KEYWORDS	AX140202.1	GI:14280541	1817 bp	DNA	linear	PAT 31-MAY-2001
SOURCE	AX140202.1	GI:14280541	1817 bp	DNA	linear	PAT 31-MAY-2001
ORGANISM	AX140202.1	GI:14280541	1817 bp	DNA	linear	PAT 31-MAY-2001
REFERENCE	AX140202.1	GI:14280541	1817 bp	DNA	linear	PAT 31-MAY-2001
AUTHORS	AX140202.1	GI:14280541	1817 bp	DNA	linear	PAT 31-MAY-2001
TITLE	AX140202.1	GI:14280541	1817 bp	DNA	linear	PAT 31-MAY-2001
JOURNAL	AX140202.1	GI:14280541	1817 bp	DNA	linear	PAT 31-MAY-2001

FEATURES		CompuGen Ltd. (IL)						
	source	Location/Qualifiers						
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ORIGIN								
Query Match 100.0%; Score 1817; DB 6; Length 1817;								
Best Local Similarity 100.0%; Pred. No. 0;								
Matches 1817; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Qy	1	GGCAATAAAGGAAACAAGCATGATTGTGAGGCACAGAGGACCGTGGACTCAGTCAG	60					
Dd	1	GGCAATAAAGGAAACAAGCATGATTGTGAGGCACAGAGGACCGTGGACTCAGTCAG	60					
Qy	61	GAGACTGGTGCTGTFCATCGCTGCCCTGGTGACTGACTTTGCTGTGTGGCCCTCAGGTGAAC	120					
Dd	61	GAGACTGGTGCTGTFCATCGCTGCCCTGGTGACTGACTTTGCTGTGTGGCCCTCAGGTGAAC	120					
Qy	121	TTACCCTCTCTGGGCCCTCATTTGTCTTAATCAATAATTAACGCTGATACCATGATATAA	180					
Dd	121	TTACCCTCTCTGGGCCCTCATTTGTCTTAATCAATAATTAACGCTGATACCATGATATAA	180					
Qy	181	ATCTGTACAGATTTCACCTGCTTCATTCCTTAACTCCCTAACCTGCTGTGAGATAAAGCGTTAAAGCGT	240					
Dd	181	ATCTGTACAGATTTCACCTGCTTCATTCCTTAACTCCCTAACCTGCTGTGAGATAAAGCGTTAAAGCGT	240					
Qy	241	CAGAGACAGTGGCATGCCAGTCCAGTGTGTCACACAGTAAGTGTGCTTAAAGCCGAGATTCAAAC	300					
Dd	241	CAGAGACAGTGGCATGCCAGTGTGTCACACAGTAAGTGTGCTTAAAGCCGAGATTCAAAC	300					
Qy	301	TCAGACCTTCTGGCCCCCTTGCTTAGGAGAGCATCCCAGTTGTCTAGCAGATTCTCTTTT	360					
Dd	301	TCAGACCTTCTGGCCCCCTTGCTTAGGAGAGCATCCCAGTTGTCTAGCAGATTCTCTTTT	360					
Qy	361	GCCTGAGTGGCCAGATGACATCTCTTTTAGAGCTAGAAAAGAGGAGAATGACACAGGG	420					
Dd	361	GCCTGAGTGGCCAGATGACATCTCTTTTAGAGCTAGAAAAGAGGAGAATGACACAGGG	420					
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Qy	481	TGTTCTGCCTTTTCATGGGAAGAGATACTCCCCCGGCGAGAGCTGGCACCCCTACTTGG	540					
Dd	481	TGTTCTGCCTTTTCATGGGAAGAGATACTCCCCCGGCGAGAGCTGGCACCCCTACTTGG	540					
Qy	541	AGCCACAAGGCGTGATGTACTGCCCTGCCTGTACTGCTCAGAGGGCCCCCATGTGAGTT	600					
Dd	541	AGCCACAAGGCGTGATGTACTGCCCTGCCTGTACTGCTCAGAGGGCCCCCATGTGAGTT	600					
Qy	601	GTTACCGCTTCGACTGTCCGCTGTCCACTGCCCCCAGCCTGTGTGACGAGCCACAGCAAT	660					
Dd	601	GTTACCGCTTCGACTGTCCGCTGTCCACTGCCCCCAGCCTGTGTGACGAGCCACAGCAAT	660					
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Dd	721	GCCAGCACAAACGGGACCATGTACCAACACGGAGAGATCTTTCAGTCCCCATGAGCTGTTC	780					
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Dd	781	CCTCCCGCTGCCCAACCAAGTGTCTCTCTGAGCTGCACAGAGGCCAGATCTCTACTGGG	840					
Qy	841	GCCTCACAACTGCCCGGAAACCAAGTGTCCCTGAGCTGCCACAGACCTCCCGCTGCCAGACTCTCTGCT	900					
Dd	841	GCCTCACAACTGCCCGGAAACCAAGTGTCCCTGAGCTGCCACAGACCTCCCGCTGCCAGACTCTCTGCT	900					

[illegible]

RESULT 2
AX140198
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

AX140198	1890 bp	DNA	linear	PAT 31-MAY-2001
Sequence 4 from Patent WO0134796.				
AX140198				
AX140198.1	GI:14280537			
Homo sapiens (human)				

AX140203	AX140203	Sequence	9	from Patent WO0134796.	1622 bp	DNA	linear	PAT 31-MAY-2001
LOCUS	AX140203	DEFINITION	9	from Patent WO0134796.	1622 bp	DNA	linear	PAT 31-MAY-2001
ACCESSION	AX140203	VERSION	1	GI:14280542				
KEYWORDS		ORGANISM		Homo sapiens (human)				
SOURCE		AUTHORS		Toporik, A., Biton, S., Savitzky, K. and Bernstein, J.				
REFERENCE		TITLE		Chordin-like homologs				
JOURNAL				Patent: WO 0134796-A 9 17-MAY-2001;				
FEATURES				CompuGen Ltd. (IL)				
source				Location/Qualifiers				
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				Best Local Similarity	89.3%;	Pred. No. 0;		
				Matches 1622;	Conservative 0;	Mismatches 0;	Indels 195;	Gaps 1;
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DB	1	GGCAAAATAAAAGGAAACAAGCATGATTGTGAGGCGAGAGGAGCTGGGGACTCAGTCAG	60					
QY	61	GAGACTGGTGCTGTCATCGCTGCTCGTGCTGACTGACTGCTGTGTGGCCCTCAGGTGAAC	120					
DB	61	GAGACTGGTGCTGTCATCGCTGCTCGTGCTGACTGACTGCTGTGTGGCCCTCAGGTGAAC	120					
QY	121	TTACCTCTCTGGGCCCTCATTTGCTTAATCATATAATTAACGCTGATACCATGATATAA	180					
DB	121	TTACCTCTCTGGGCCCTCATTTGCTTAATCATATAATTAACGCTGATACCATGATATAA	180					
QY	181	ATCTGTACAGCATTTCACTGCTTCATTCCCTAACTGCCCTGTGAGATAAGCGTTAAAGCT	240					
DB	181	ATCTGTACAGCATTTCACTGCTTCATTCCCTAACTGCCCTGTGAGATAAGCGTTAAAGCT	240					
QY	241	CAGAGACAGTGGCATGCCCAGTGTTCACAGTAAAGTGTGGTAAAGCCGAGATTCAAAC	300					
DB	241	CAGAGACAGTGGCATGCCCAGTGTTCACAGTAAAGTGTGGTAAAGCCGAGATTCAAAC	300					
QY	301	TCAGACCTTCTGGGCCCTTGGCTTAGGAGAGCATGCCAGTTGCTAGCAGATTCTCTTTT	360					
DB	301	TCAGACCTTCTGGGCCCTTGGCTTAGGAGAGCATGCCAGTTGCTAGCAGATTCTCTTTT	360					
QY	361	GCCTGAGTGGCCCCAGATGACATCTCTTTTAGAGCTAGAAAAGAGAGAAATGAGACAGG	420					
DB	361	GCCTGAGTGGCCCCAGATGACATCTCTTTTAGAGCTAGAAAAGAGAGAAATGAGACAGG	420					
QY	421	TCCTTTGGGCTGGAGCCTCCTGGGACTAAACATGGCAGCTGGTCCGTTTGGCAGGCCAGACA	480					
DB	421	TCCTTTGGGCTGGAGCCTCCTGGGACTAAACATGGCAGCTGGTCCGTTTGGCAGGCCAGACA	480					
QY	481	TGTTCTGCCTTTTTCATGGGAAGAGATGATCTCCCGGCGAGAGCTGGGACCCCTACTTGG	540					
DB	481	TGTTCTGCCTTTTTCATGGGAAGAGATGATCTCCCGGCGAGAGCTGGGACCCCTACTTGG	540					
QY	541	AGCCACAGGGCTGATGACTGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	600					
DB	541	AGCCACAGGGCTGATGACTGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	600					
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DB	601	GTTACCGGCTCCACTGTCGGCTGTCCACTGCGCCCGCAGCTGTGACGGAGCCACAGCAAT	660					
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 1264 TGACCTGTCCACCGAGTACCTCCCTGCTGACCCCGAGAAAGTGGTGGAAAGTGTGCTGCA 1323
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 1804 CATACCATCAAAA 1817
 1709 CATACCATCAAAA 1722

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 VERSION AX119273.1 GI:14036224
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Turner,C.A., Donoho,G., Nehls,M., Hilbun,B., Zambrowicz,B. and
 Sands,A.T.
 TITLE Human proteins and polynucleotides encoding the same

1801 TTGCATAACCATCAAAA 1817
 1606 TTGCATAACCATCAAAA 1622
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 VERSION AX140200.1 GI:14280539
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 SOURCE Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Toporoff,A., Biton,S., Savitzky,K. and Bernstein,J.
 TITLE Chordin-like homologs
 JOURNAL Patent: WO 0134796-A 6 17-MAY-2001;
 Compugen Ltd. (IL)
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 /db_xref="taxon:9606"
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 Best Local Similarity 97.8%; Pred. No. 0;
 Matches 1363; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
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 604 ACCGCTTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
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 629 AGCAACAGGAGCCATGTACCAACAGGAGAGATCTTCAAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCT 688
 784 CCGGCT 843
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JOURNAL Patent: WO 0129084-A 5 26-APR-2001;
Lexicon Genetics Incorporated (US)
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VERSION AX048199.1 GI:11876989
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1
AUTHORS Tang,Y.T., Yue,H., Lal,P., Burford,N., Bandman,O., Baughn,M.R.,
Azimzai,Y., Lu,D.A. and Patterson,C.
TITLE Extracellular signaling molecules
JOURNAL Patent: WO 0070049-A 39 23-NOV-2000;
Incye Genomics, Inc. (US)
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REFERENCE	1		
AUTHORS	Eaton,D.L., Filvaroff,E., Gerritsen,M.B., Goddard,A., Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and Wood,W.I.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: WO 0116318-A 81 08-MAR-2001; Genentech, Inc. (US)		
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SEQUENCE 141 from Patent WO0078961.
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AX697073.1 GI:29498046
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ferrara, N., Stewart, T.A., Williams, P.M., Baker, K.P., Desnovers, L.,
Eaton, D.L., Gao, W.O., Pan, J., Botstein, D., Pong, S., Goddard, A.,
Godowski, P.J., Gurney, A.L., Smith, V., Tamas, D., Wood, W.J.,
Grimaldi, C.J., Hillan, K.J., Paoni, N.F., Roy, M.A., and Watanabe, C.K.
Secreted and transmembrane polypeptides and nucleic acids encoding

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Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
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RESULT 10

AX363203

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

Alvarez, E., McEntire, J.K., Smith, R.C. and Su, E.W.

Nucleic acids, vectors, host cells, polypeptides, and uses thereof

Patent: WO 0208277-A 5 31-JAN-2002;

ELI LILLY AND COMPANY (US)

Location/Qualifiers

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FEATURES

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 Sequence 5 from Patent WO0134796.
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 AX140199.1 GI:14280538
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 Toporok A., Biton S., Savitzky K. and Bernstein J.
 Chordin-like homologs
 Patent: WO 0134796-A 5 17-MAY-2001;
 Compugen Ltd. (IL)
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AX140204

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS:

SOURCE

ORGANIS

LOCUS AX119269 1356 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 1 from Patent WO0129084.
ACCESSION AX119269
VERSION AX119269.1 GI:14036222
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Turner C.A., Donoho, G., Nehls, M., Hilbun, E., Zambrowicz, B. and
Sands, A.T.
TITLE Human proteins and polynucleotides encoding the same
JOURNAL Patent: WO 0129084-A 1 26-APR-2001;
Lexicon Genetics Incorporated (US)
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LOCUS AX140195
DEFINITION Sequence 1 from Patent WO0134796.
ACCESSION AX140195
VERSION AX140195.1 GI:14280534
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Toporoff, A., Biton, S., Savitzky, K. and Bernstein, J.
TITLE Chordin-like homologs
JOURNAL Patent: WO 0134796-A 1 17-MAY-2001;
CompuGen Ltd. (IL)
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 ACCESSION AX363199
 VERSION AX363199.1 GI:18695336
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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 Alvarez, E., Mcentire, J.K., Smith, R.C. and Su, E.W.
 Nucleic acids vectors, host cells, polypeptides, and uses thereof
 Patent: WO 0208277-A 1 31-JAN-2002;
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RESULT 22
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TITLE
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REMARK
COMMENT

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BC019399
BC019399.1 GI:18044155
MGC.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1516)
Straussberg, R.
Direct Submission
Submitted (19-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: ang@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 41 Row: a Column: 24

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Location/Qualifiers
1. .1516

CDS

Query Match 41.3%; Score 750.8; DB 10; Length 1516;

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738	Db	GGAGAGGCCCCAGCAGCGCCAGCCCGCCAGCTCCGCTCAGCTCCCTCTGGGCTTCATCCCTC	797
1072	Qy	GCACCTTCAGACCCAAAGGAGCAGGACCAAACTGTCGAAGATCGTCTGAAGAGGAAAC	1131
798	Db	GCACCTTCAGTCAGTAGGAATGGGAGCACAACCATCAAGATTATCTTGAAGGGAAC	857
1132	Qy	ATAAAGAACCTGTGTGATGCGCGGAAGACGTACTCCACGGGAGGTGTGCACCCGG	1191
858	Db	ATAAAAAAGCTTGACACACAAATGGGAAGACATACTCCCATGGGAGGTGTGCACCCCA	917
1192	Qy	CGTTCGGTGCCTTCGGGCCCTTGCCTTGCATCTGATGACCTGTGAGGATGGCCGCCAG	1251
918	Db	CTGTGCTCTCTCTTTGGCCCCATGCCCTGCATCCTGTGCACATGTATCGATGGCTACCAG	977
1252	Qy	ACTGCGAGCTGTGACCTGTGCCACCGAGTACCCCTGCGCTCACCCCGAGAAAGTGGCTG	1311
978	Db	ACTGCCACCGTGTGACCTGCCCCACCCCAATATCCCTGCAGTCAACCCAGAAAGTGGCTG	1037
1312	Qy	GGAACTGTCTCAAGATTTTCCCGAGAGGACAAAGCAGAGCCCTGGCCACAGTGAAGTCA	1371
1038	Db	GGAACTGTCTCAAGATCTGCCCAGAGGACGAGCGGAGAGATGACACAGTGAAGTCA	1097
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1098	Db	CCACCGGTGTCCCAAGGTACCCAGGCCAGTTCATGTGTACACGTTGGCATCTCCAAGCC	1157
1432	Qy	CAGACAACTCGGTGCTTTTGGCTTGGACACGAGGCCCTCGGACTTGTGGAGATCTACC	1491
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1492	Qy	TCTGGAAGCTGTAAAGATGAGGAAACTGAGGCTCAGAGAGGTGAAGTACCTGGGCCAA	1551
1218	Db	TTTGAAGCTGTGAAG-----	1235
1552	Qy	GGCCACAGCCAGAACTTTCACCTTGACTCAGATCAAGAAAGTCAGGAAGCAAGCTTC	1611
1236	Db	-----GAATCTACCACTTGTTTCAGATCAAGAGAGTCAGGAAGCAAGATTC	1282
1612	Qy	CAGAAAGGACACAGCACTTCGGACTGCTCGTGGCCCCCAGAGAGTCACTGGAACTGC	1671
1283	Db	CAGAAAGAGGTTCAGAACTTCGGGTGCTCTACCGGCACCCCATGAAGGTTACTGGCCG	1342
1672	Qy	TTCTTAGCCCCAGACCTCGAGCTGAAGGTCAAGGTCAGGCGAGTCCAGACAAAGTGACCAAGACA	1731
1343	Db	TTCTTAGCCCCAGACTCCAGAGCTGAAGTTACAGCCAGCCACAGCAAAAGTGACCAAGACA	1402
1732	Qy	TAACAAGA-----CCTAACAGTTGCAGATATGAGCTGTATAATTTGTTTATATATTT	1787
1403	Db	TTATAGCAAGGACCTTAAGAGTTGCAGATACGAGTTTATTCGTTTGTATATATTT	1462
1788	Qy	AATAAATGAAGTTGCATAACCATCAAAA	1817
1463	Db	AATA-----AAGAAGTCGCATTACCTTCAAAA	1489

RESULT 23
AX235833

Accession	AX235833	1839 bp	linear	PAT 26-SEP-2001
LOCUS	AX235833			
DEFINITION	Sequence 1 from Patent WO0164885.			
ACCESSION	AX235833			
VERSION	AX235833.1	GI:15795737		

KEYWORDS	.	Mus musculus (house mouse)
SOURCE		Mus musculus
ORGANISM		Mus musculus

ORGANISM

REFERENCE
1 Zhang, K., Linh, C. and Nakayama, N.
AUTHORS
TITLE Chordin-like-2 molecules and uses thereof
JOURNAL Patent: WO 0164885-A 1 07-SEP-2001;
Amgen Inc. (US)

FEATURES	Location/Qualifiers
Amgen Inc. (US)	

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RESULT 24
AF338222
LOCUS      1428 bp      mRNA      linear      ROD 05-MAY-2001
DEFINITION Mus musculus chordin-related protein neuralin-2 mRNA, complete cds.
ACCESSION AF338222
VERSION    AF338222.1  GI:13957540
KEYWORDS
SOURCE     Mus musculus (house mouse)
ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 1428)
            Coffinier,C.C. and De Robertis,E.M.
            Direct Submission
            Submitted (17-JAN-2001) Biological Chemistry, UCLA - HEMI, 675
            Charles E. Young Drive S, Los Angeles, CA 90095-1662, USA
FEATURES
            Location/Qualifiers
                1..1428
                    /organism="Mus musculus"
                    /mol_type="mRNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /chromosome="7"
                    /dev_stage="embryo E8.5"
                    /note="similar to sequence deposited with GenBank
                    Accession Number A110168"
                67..1428
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                    CDS

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772	AGCTGTTCCCTCCGCTCCGCAACCCAGTGTGCTCTGCAGTGCACAGAGGCCAGA	831
853	AGCTGTTCCCTCCGCTCCGCTCCAACACAGTGTGCTGTAGCTGTATTGAAGGCCACA	912
832	TCTACTGGGGCTCACAACCTGCCCGAAACAGGCTGCCAGCACCCCTCCCGTGCAG	891
913	CTTACTGTGGTCTCATGACCTGTCTGMAACCGAGCTGCCCCACACACTCCCTCTGCCTG	972
892	ACTCCTGCTGCCAAGCCTCAAAGATGAGGCAAGTGAGCAATCGATGAAGAGGACAGTG	951
973	ATTCTGTGTCAGACCTCAAAGACAGGACAACTGAGAGTTCCACAGAAAGAACTTGA	1032
952	TGCAGTGCCTCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAA	1011
1033	CACAGCTGCAGCATGSAGAGAGACATTCGCCAGGATCCATGCTC-----GGAGA	1080
1012	AGAGAGGCCCGGGACCCGAGCCCCCACTGGCCTCAGGCCCCCTCTGAGCTTCATCCCTC	1071
1081	GGAGAGGCCCGGACGACGCGAGCCCCACACAGCCTCAGCTCCCTCTGGGCTTCATCCCTC	1140
1072	GCCACITTCAGACCCCAAGGGAGCAGGCGACCAACTGTCAAGATCGTCTGTGAGGAGAAAC	1131
1141	GCCACTTCAGTCAGTAGGAATGGGCAGCACCACTCAAGATTATCTTGAAGGAGAAAC	1200
1132	ATAAGAAAGCCTGTGTCATGGCGGGAAGACGTACTCCGAGGGGAGGTGTGGCACCCGG	1191
1201	ATAAAAAAGCTTGCACACACAATGGGAAGACATACTCCCATGGGAGGTGTGGCACCCCA	1260

RESULT 27	LOCUS	DEFINITION	AP001324	230157 bp	DNA	linear	PRI 24-JAN-2002
AP001324/c	LOCUS	DEFINITION	Homo sapiens genomic DNA, chromosome 11q clone:RP11-864N7, complete sequences.				
ACCESSION	AP001324	HTG	AP001324.4 GI:18307724				
VERSION	AP001324	HTG	Homo sapiens (human)				
KEYWORDS	AP001324	HTG	Homo sapiens				
SOURCE	AP001324	HTG	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
ORGANISM	AP001324	HTG	Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.				
REFERENCE	AP001324	HTG	Homo sapiens genomic DNA				
AUTHORS	AP001324	HTG	Published Only in Database (2000)				
TITLE	AP001324	HTG	2 (bases 1 to 230157)				
JOURNAL	AP001324	HTG	Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.				
COMMENT	AP001324	HTG	Submitted (01-WAR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Japan				
FEATURES	AP001324	HTG	1-2-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)				
BASE COUNT	AP001324	HTG	On Jan 23, 2002 this sequence version replaced gi:10130051.				
ORIGIN	AP001324	HTG	Location/Qualifiers				
Query Match	AP001324	HTG	1. 230157				
Best Local Similarity	AP001324	HTG	/organism="Homo sapiens"				
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	AP001324	HTG	/mol_type="genomic DNA"				
	AP001324	HTG	/db_xref="taxon:9606"				
	AP001324	HTG	/chromosome="11"				
	AP001324	HTG	/map="11q"				
	AP001324	HTG	/clone="RP11-864N7"				
	AP001324	HTG	63975 a 48485 c 51746 g 65951 t				
1	GGACAATAAAAGGAACAAGCATGATTGTGAGGGCAGAGAGCGTGGGACTGAGTCAG	60					
98435	GGACAATAAAAGGAACAAGCATGATTGTGAGGGCAGAGAGCGTGGGACTGAGTCAG	98376					
61	GAGACTGGTGCTGTCATCGCTCGCTGCTGAGTGAAGTGTGTCGTGTGCGCCCTCAGGTGTAAC	120					
98375	GAGACTGGTGCTGTCATCGCTCGCTGCTGAGTGAAGTGTGTCGTGTGCGCCCTCAGGTGTAAC	98316					
121	TTACCCCTCTCTGGGCGCTCATTTGCTCAATCAATAATTAACGCTGATACCATGATATAA	180					
98315	TTACCCCTCTCTGGGCGCTCATTTGCTCAATCAATAATTAACGCTGATACCATGATATAA	98256					
181	ATCTGTACAGCATTTTCACTGCTTGAATTCCTTAACCTGCTGTGAGATAAGCGTTAAGGCT	240					
98255	ATCTGTACAGCATTTTCACTGCTTGAATTCCTTAACCTGCTGTGAGATAAGCGTTAAGGCT	98196					
241	CAGAGACAGTGGCATGCCAGTGTTCACAGTAAGTGTGTGTAAGCCGAGATTCAAC	300					
98195	CAGAGACAGTGGCATGCCAGTGTTCACAGTAAGTGTGTGTAAGCCGAGATTCAAC	98136					
301	TCAGACCTTCTGGCCCTTCGCTAGGAGAGCATGCCAGTGTCTAGCAGATTCTCTTTT	360					
98135	TCAGACCTTCTGGCCCTTCGCTAGGAGAGCATGCCAGTGTCTAGCAGATTCTCTTTT	98076					
361	GCTGTAGTGCCTCAGATGACATCTCTTTTAGAGCTAGAAAAGAGGAAGTAATGACAGGG	420					
98075	GCTGTAGTGCCTCAGATGACATCTCTTTTAGAGCTAGAAAAGAGGAAGTAATGACAGGG	98016					
421	TCTTTGGGCTGGAGCCCTCCTGGGACTAACATGGCACTGCTCGGTTTGCAGGCCACACA	480					

RESULT 27	LOCUS	DEFINITION	AP001324	230157 bp	DNA	linear	PRI 24-JAN-2002
AP001324/c	LOCUS	DEFINITION	Homo sapiens genomic DNA, chromosome 11q clone:RP11-864N7, complete sequences.				
ACCESSION	AP001324	HTG	AP001324.4 GI:18307724				
VERSION	AP001324	HTG	Homo sapiens (human)				
KEYWORDS	AP001324	HTG	Homo sapiens				
SOURCE	AP001324	HTG	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
ORGANISM	AP001324	HTG	Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.				
REFERENCE	AP001324	HTG	Homo sapiens genomic DNA				
AUTHORS	AP001324	HTG	Published Only in Database (2000)				
TITLE	AP001324	HTG	2 (bases 1 to 230157)				
JOURNAL	AP001324	HTG	Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.				
REFERENCE	AP001324	HTG	Direct Submission				
AUTHORS	AP001324	HTG	Submitted (01-WAR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Japan				
TITLE	AP001324	HTG	1-2-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan				
JOURNAL	AP001324	HTG	(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)				
COMMENT	AP001324	HTG	On Jan 23, 2002 this sequence version replaced gi:10130051.				
FEATURES	AP001324	HTG	Location/Qualifiers				
SOURCE	AP001324	HTG	1. 230157				
BASE COUNT	AP001324	HTG	/organism="Homo sapiens"				
ORIGIN	AP001324	HTG	/mol_type="genomic DNA"				
	AP001324	HTG	/db_xref="taxon:9606"				
	AP001324	HTG	/chromosome="11"				
	AP001324	HTG	/map="11q"				
	AP001324	HTG	/clone="RP11-864N7"				
	AP001324	HTG	63975 a 48485 c 51746 g 65951 t				
Query Match	AP001324	HTG	32.2%; Score 595; DB 9; Length 230157;				
Best Local Similarity	AP001324	HTG	100.0%; Pred. No. 1.1e-146;				
Matches	AP001324	HTG	585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
1	GGACAATAAAAGGAACAAGCATGATTGTGAGGGCAGAGAGCGTGGGACTGAGTCAG	60					
98435	GGACAATAAAAGGAACAAGCATGATTGTGAGGGCAGAGAGCGTGGGACTGAGTCAG	98376					
61	GAGACTGGTGCTGTCATCGCTCGCTGCTGAGTGAAGTGTGTCGTGTGCGCCCTCAGGTGTAAC	120					
98375	GAGACTGGTGCTGTCATCGCTCGCTGCTGAGTGAAGTGTGTCGTGTGCGCCCTCAGGTGTAAC	98316					
121	TTACCCCTCTCTGGGCGCTCATTTGCTCAATCAATAATTAACGCTGATACCATGATATAA	180					
98315	TTACCCCTCTCTGGGCGCTCATTTGCTCAATCAATAATTAACGCTGATACCATGATATAA	98256					
181	ATCTGTACAGCATTTTCACTGCTTGAATTCCTTAACCTGCTGTGAGATAAGCGTTAAGGCT	240					
98255	ATCTGTACAGCATTTTCACTGCTTGAATTCCTTAACCTGCTGTGAGATAAGCGTTAAGGCT	98196					
241	CAGAGACAGTGGCATGCCAGTGTTCACAGTAAGTGTGTGTAAGCCGAGATTCAAAC	300					
98195	CAGAGACAGTGGCATGCCAGTGTTCACAGTAAGTGTGTGTAAGCCGAGATTCAAAC	98136					
301	TCAGACCTTCTGGCCCTTCGCTAGGAGAGCATGCCAGTGTCTAGCAGATTCTCTTTT	360					
98135	TCAGACCTTCTGGCCCTTCGCTAGGAGAGCATGCCAGTGTCTAGCAGATTCTCTTTT	98076					
361	GCTGTAGTGCCTCAGATGACATCTCTTTTAGAGCTAGAGAGAGGAGGAATGAGACAGGG	420					
98075	GCTGTAGTGCCTCAGATGACATCTCTTTTAGAGCTAGAGAGAGGAGGAATGAGACAGGG	98016					
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Db 97955 TGTTCCTGCTTTTCCATGGGAAGAGATACCTCCCGCGGAGAGCTGCGACCCCTACTTGG 97956
Qy 541 AGCCACAGGCTGATGTACTGCTCGGCTGTACCTGCTCAGAGG 585
Db 97895 AGCCACAGGCTGATGTACTGCTCGGCTGTACCTGCTCAGAGG 97851

RESULT 28
AF002010
LOCUS Homo sapiens chromosome 11 clone RP11-880P3 map 11q14, WORKING
DEFINITION DRAFT SEQUENCE, 34 unordered pieces.
ACCESSION AP002010.2 GI:8117625
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 11452)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Tokoki, Y., Watanabe, H. and Sakaki, Y.
Homo sapiens 211,452 genomic DNA of 11q14
Published Only in Database (2000)
TITLE Homo sapiens 211,452 genomic DNA of 11q14
JOURNAL
REFERENCE 2 (bases 1 to 211452)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Tokoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (08-MAY-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
Japan (E-mail:hattori@gsc.riken.go.jp,
URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
On May 30, 2000 this sequence version replaced gi:7768935.
----- Genome Center
Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: Humbrat11
Center clone name: RP11-880P3
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 189257 bases at least Q40
Consensus quality: 200319 bases at least Q30
Consensus quality: 205564 bases at least Q20
Insert size: 208152; sum-of-contigs
Quality coverage: 4.07x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved
1 28021 contig of 28021 bp in length
28122 42064 contig of 13943 bp in length
42165 54544 contig of 12380 bp in length
54645 69334 contig of 12290 bp in length
69335 78065 contig of 11031 bp in length
78066 85965 contig of 7800 bp in length
85966 94021 contig of 7956 bp in length
94022 94121 contig of 100 bp in length
94122 103137 contig of 9016 bp in length
103138 103237 gap of 100 bp
103238 110428 contig of 7191 bp in length
110429 110528 gap of 100 bp
110529 117261 contig of 6733 bp in length
117262 117361 gap of 100 bp
117362 124135 contig of 6774 bp in length
124136 124236 gap of 100 bp
124236 130599 contig of 6364 bp in length
130600 130699 gap of 100 bp
130700 136620 contig of 5921 bp in length
136621 136720 gap of 100 bp
136721 143251 contig of 6531 bp in length
143252 143351 gap of 100 bp
143352 149360 contig of 6009 bp in length
149361 149361 gap of 100 bp
149361 154913 contig of 5353 bp in length
154914 154914 gap of 100 bp
154914 160814 contig of 5901 bp in length
160815 160914 gap of 100 bp
160915 165830 contig of 4916 bp in length
165831 165930 gap of 100 bp
165931 171277 contig of 5347 bp in length
171278 171377 gap of 100 bp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 34 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

Query Match 31.6%; Score 574; DB 2; Length 211452;
Best Local Similarity 100.0%; Pred. No. 1.1e-143;
Matches 574; Conservative 0; Mismatches 0; Indels 0;


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2Y 1787 TAATAAATAAG 1797
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2b 1177 TAATAAGAAG 1187

RESULT 31
LOCUS AX014296 422 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 4 from Patent WO9954353.
ACCESSION AX014296
VERSION AX014296.1 GI:10040650
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and
Pilarczyk,C.
TITLE Human nucleic acid sequences of normal uterus tissue
JOURNAL Patent: WO 9954353-A 4 28-OCT-1999;
SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN
(DE); PILARSKY CHRISTIAN (DE)
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source
location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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BASE COUNT 130 a 115 c 96 g 81 t
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Best Local Similarity 97.1%; Pred. No. 5.9e-85;
Matches 374; Conservative 0; Mismatches 8; Indels 3; Gaps 1;
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1Y 1493 CTGGAAGCTGTAAAGATGAGGAACCTGAGGCTCAGAGAGTGAAGTACCTGGGCCAAG 1552
2b 98 CTGGAAGCTGTAAAGATGAGGAACCTGAGGCTCAGAGAGTGAAGTACCTGGGCCAAG 157
1Y 1553 GCCACACAGCAGAGATCTCCACTTGACTCAGATCAAGAACTCAGGAAGCAAGCTTCC 1612
2b 158 GCCACACAGCAGAGATCTCCACTTGACTCAGATCAAGAACTCAGGAAGCAAGCTTCC 217
1Y 1613 AGAAAGGACACAGCACTTCGAGCTGCTCGTGGCCGCCACCAAGGTCACTGGAAGCTCT 1672
2b 218 AGAAAGGACACAGCACTTCGAGCTGCTCGTGGCCGCCACCAAGGTCACTGGAAGCTCT 277
1Y 1673 TCCTAGCCCGACCTGAGCTGAAGGTCAAGGCTCAGAGAGTCAAGTGAAGTGAAGTCAAT 1732
2b 278 TCCTAGCCCGACCTGAGCTGAAGGTCAAGGCTCAGAGAGTCAAGTGAAGTGAAGTCAAT 337
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2b 338 AACAAAGACCTAACAGTTCAGATGATGAGTGTATAATTTGTTATTATATATATAA 397
1Y 1793 ATAAGAAGTGCATACCAATCAAAA 1817
2b 398 ATAAGAAGTGCATACCAATCAAAA 422

RESULT 32
LOCUS AX337465/c 421 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 7974 from Patent WO0194629.
ACCESSION AX337465
VERSION AX337465.1 GI:18128184
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Nakayama,N., Wen,D., Han,C.Y., He,C. and Yu,D.
TITLE Chordin-like molecules and uses thereof
JOURNAL Patent: WO 0142465-A 4 14-JUN-2001;
Angen Inc. (US)
FEATURES
source
location/Qualifiers
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/db_xref="taxon:9606"
BASE COUNT 81 a 111 g 130 t 4 others
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Best Local Similarity 96.4%; Pred. No. 9.8e-81;
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1Y 1494 TGAAGCTGTAAAGATGAGGAACCTGAGGCTCAGAGAGTGAAGTGAAGTGAAGTGAAGT 1553
2b 323 TGAAGCTGTAAAGATGAGGAACCTGAGGCTCAGAGAGTGAAGTGAAGTGAAGTGAAGT 265
1Y 1554 CCACACAGCCAGAACTTCCACTTGACTCAGATCAAGAACTCAGGAAGCAAGCTTCCA 1613
2b 264 CCACACAGCCAGAACTTCCACTTGACTCAGATCAAGAACTCAGGAAGCAAGCTTCCA 205
1Y 1614 GAAAGAGCAGAGACTTCCGACTGCTCGTGGCCGCCACCAAGGTCACTGGACGCTTT 1673
2b 204 GAAAGAGCAGAGACTTCCGACTGCTCGTGGCCGCCACCAAGGTCACTGGACGCTTT 145
1Y 1674 CCTAGCCCGACCTTGGAGCTGAAGGTCAAGGCTCAGAGAGTGAAGTGAAGTGAAGTGAAGT 1733
2b 144 CCTAGCCCGACCTTGGAGCTGAAGGTCAAGGCTCAGAGAGTGAAGTGAAGTGAAGTGAAGT 85
1Y 1734 ACAAGAGCTTAACAGTTGAGATATGAGCTGTATATTTGTTATTATATATATAA 1793
2b 84 ACAAGAGCTTAACAGTTGAGATATGAGCTGTATATTTGTTATTATATATATAA 25
1Y 1794 TAAGAAGTGCATACCAATCAAAA 1817
2b 24 TAAGAAGTGCATACCAATCAAAA 1
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LOCUS AX175123 3827 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 4 from Patent WO0142465.
ACCESSION AX175123
VERSION AX175123.1 GI:14598541
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1
AUTHORS Nakayama,N., Wen,D., Han,C.Y., He,C. and Yu,D.
TITLE Chordin-like molecules and uses thereof
JOURNAL Patent: WO 0142465-A 4 14-JUN-2001;
Angen Inc. (US)
FEATURES
source
location/Qualifiers
1..3827
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BASE COUNT 81 a 111 g 130 t 4 others
ORIGIN
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Best Local Similarity 53.3%; Pred. No. 1.4e-45;
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DB 587 CTACTGGAACCGTATGAGCTGGTTTACTGTGAACTGCATCTGTCTCAGAAATGGAA 646
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QY 713 AAAGTCTGCGCAGACACACGAGCAGTATGACCAACACGAGAGATCTTCACTGCCCCATGA 772
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QY 1181 GTGCAACCGGCTTTCGCTGCTTCCGCTTTCCTGCTCATCTGACCTGTGAGGA 1240
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QY 1241 TGGCGCGCAGGACTGCCAGCGTGTGACCTGTCCACCGAGTACCTTCCGCTGACCCCGA 1300
DB 1307 CACCAAGCAAGATGTAAAGAAATCCACTGCCCCCAATCGATACCTCCCTGCAAGTATCTCA 1366
QY 1301 GAAAGTGTGGGAGTGTCTGCAAGATTTGCCAGAGGCAAGAGACAGCTG 1353
DB 1367 AAAAATAGATGAAAGTGTCTCAAGGTGTGCCAGGTGAGGCAAGGCAAGAGTGT 1419

588 ATACTGTGGTCTCAAGACTTCCCAAACTGACCTGTGATTCATCCAGTCTCTGTTCCAGA 647
893 CTCTGCTGCGCAAGCTTCAAGATGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 952
648 TTCTTGTGCGGAGTATGAGAGGGGATGCAAGATTTATGCTGGGAACATGCGGATGGTA 707
953 GCAGTCTGCTCA-----TGGGCTGAGACATCTCAGGATCCATGTTCCAGTGA 1000
708 TATCTTCCGCAACTGCCACAGAGAGACAGACATCTTACTCTCGTTCCTCCCTACGA 767
1001 TGTGGGAGAAAGAGAGCGCCGCGCACCCAGCCCCCACTGGCCTCAGCGCCCTCTGAG 1060
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948 CTGGCAACCAATCTACAGCATTTGGCATTTGGAATGTGACTATGACATTTGTATGT 1007
1241 TGGCGCGCAGGACTGCCAGCGTGTGACCTGTCCACCGAGTACCCCTGCGCTCACCCGA 1300
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AF296451
AF296451.1 GI:14625825
MUS MUSCULUS (HOUSE MOUSE)
MUS MUSCULUS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3291)
Sakuta, H., Suzuki, R., Takahashi, H., Kato, A., Shintani, T.,
Iemura, S., Yamamoto, T. S., Ueno, N. and Noda, M.
Ventroptin: a BMP-4 antagonist expressed in a double-gradient
pattern in the retina
Science 293 (5527), 111-115 (2001)
21334726
MEDLINE
11441185
PUBMED
2 (bases 1 to 3291)
Sakuta, H. and Noda, M.
Direct Submission
Submitted (16-AUG-2000) Division of Molecular Neurobiology,
National Institute for Basic Biology, 38 Nishigonaka, Myodaiji-cho,
Okazaki, Aichi 444-8585, Japan
Location/Qualifiers
i. 3291
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441  ATACTGTGTCTCAAGACTTGGCCCAAACTGACCTGTGTCAATTCCTCCAGTCTCTGTCCAGA 500
893  CTCCTGCTGCCAAGCCTGCAAGATCAGGCAAGTGAAGCAATCGGATGAAGAGACAGTGT 952
501  TTCTTCTGTCGCGAGTATGCAGAGGGGATGCAGAAATATCGTGGGAACATCGGATGGTGA 560
953  GCAGTCGCTCCCA-----TGGGGTGAGACATCCTCAGGATCCATGTITCCAGTGA 1000
561  TATCTTCGGCAACCTGCCAACAGAGAAGCAGACATTTTACCTCCGTTCCCTCCCTACGA 620
1001  TGCTGGGAGAAAGAGAGGCGCCGGGCACCCAGCCCCCACTGGGCTCAGCGCCCTCTGAG 1060
621  TCCTCCACCAACACAGACAGCTGGAGTCTTCCCGCTTCTCTGGGAGCAGAAAGTCAACG 680
1061  CTTTCATCCTCCGCACTTCAGACCCCAAGGAGCAGCAGCAACAATGTCGAAGATCTGCTCT 1120
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1121  GAAGGAGAAACATAGAAAGCCTGTGTGATGGCGGAAGACGTACTCCACCGGGAGGT 1180
741  CAAGCACAAACATGGACAAGTGTGTGTTTCCAAATGGAAGACCTACTCTCATGGAGATC 800
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801  CTGGCACCCAAATCTACGAGCATTTGGCAATGTGGAAATGTGTACTATGCATTTGTAATGT 860
1241  TGCGCGCCAGGACTGCACGGTGTGACCTGTCCACCGAGTACCCCTGCCGTCAACCCCGA 1300
861  CACCAGCAAGATGTAGAAATAATCACTGCCCAATCGATACCCCTGCAAGTATCCTCA 920
1301  GAAAGTGGCTGGGAAGTGTGCAAGATTTGCCCAGAGGA 1339
921  AAAAAATAGATGAAAGTGTGCAAGTGTGCCCAGAGA 959

RESULT 37
BC050818
LOCUS
DEFINITION Mus musculus cDNA clone IMAGE:511005, partial cds.
ACCESSION BC050818
VERSION BC050818.1 GI:30046942
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3601)
Strausberg R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Zdobych, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Altschul, S.F., Jordan, B., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Hopkins, R.F., Jorde, M., Fink, A., Lander, E.S., Lander, E.S., Lander, E.S.,
Diatchenko, L., Marusina, K., Fink, A., Rubin, G.M., Hong, L.,
Diatchenko, L., Marusina, K., Fink, A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldi, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E.,
Schnurch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
2398257

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12477932
2 (bases 1 to 3601)
PUBLISHED
REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (09-APR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
BC Cancer Agency, Vancouver, BC, Canada
info@bcsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smalus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 13752588.
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mesenchyme and early condensing mesenchyme."
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Matches 469; Conservative 0; Mismatches 396; Indels 12; Gaps 1;
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y 533 CTACTTGGAGCCACAGGCTGTATGTACTGCTCGCTGTACTGTCTCAGAGGGGCCCA 592
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y 713 AAAGTCTCCAGCAACAGGGACCATGTATACCAACAGGAGAGATCTTCACTGCCCATGA 772
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QY 953 GCAGTGCCTCCA-----TGGGGTGCAGACATCTCAGGATCCATGTTCCAGTGA 1000
Db 575 TATCTTCCGGCAACCTGCCAACAGAGAGCAAGACATTTCTTACCTCCGTTCCCGCTACGA 634
QY 1001 TGTCTGGAGAAAGAGAGCGCCGGCACCCAGCCCCCTGCGCTCAGCGCCCTCTGAG 1060
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VERSION
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AUTHORS
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MEDLINE
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AUTHORS
TITLE
JOURNAL
FEATURES
source
Mus musculus (house mouse)
Mus musculus
Mus musculus neuralin mRNA, complete cds.
AF305714.1 GI:11037011
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Coffinier, C., Tran, U., Larrain, J. and De Robertis, E.M.
Neuralin-1 is a novel Chordin-related molecule expressed in the
mouse neural plate
Mech. Dev. 100 (1), 119-122 (2001)
20568969
11118896
2 (bases 1 to 2750)
Coffinier, C. and De Robertis, E.M.
Direct Submission
Submitted (14-SEP-2000) Biological Chemistry, HHMI-UCLA, 675 Young
Drive S, Los Angeles, CA 90095-1662, USA
Location/Qualifiers
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BC002909	2497 bp	mRNA	linear	PRI 12-JUL-2001
LOCUS				
DEFINITION	Homo sapiens, similar to chordin-like, clone MGC:11264			
IMAGE	IMAGE:3942645, mRNA, complete cds.			
ACCESSION	BC002909			
VERSION	BC002909.1			
GI	GI:12804112			
KEYWORDS	MGC.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
DATA_1	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
DATA_2	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 2497)			
AUTHORS	Strausberg,R.			
TITLE	Direct Submission			
JOURNAL	Submitted (05-FEB-2001) National Institutes of Health, Mammalian			
GENE	Gene Collection (MGC), Cancer Genomics Office, National Cancer			
INSTITUTE	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,			
USA	USA			
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov			

REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: cgapps-remail.nih.gov Tissue Procurement: DCTD/DTP cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC) Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc_mgc@ncgri.nih.gov Shvachenko, Y., Wetherby, R.D., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R., Lim, M., Maduro, Q.L., Masiello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantipop, S., Thomas, P.J., Tongson, E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Zhang, L.-H. and Green, E. D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL plate: 15 Row: 0 Column: 13
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

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source

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Matches 469; Conservative 0; Mismatches 405; Indels 12; Gaps 1;

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RESULT 40
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Sequence 7 from Patent WO0142465.
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AX175126.1 GI:14598543
EYWORDS
Homo sapiens (human)

AX175126 1496 bp DNA linear PAT 03-JUL-2001

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 Nakayama, N., Wen, D., Han, C. Y., He, C. and Yu, D.
Chordin-like molecules and uses thereof
Patent: WO 0142465-A 7 14-JUN-2001;
Amgen Inc. (US)

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Query Match 11.0%; Score 199; DB 6; Length 1496;
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Matches 474; Conservative 0; Mismatches 400; Indels 15; Gaps 2;

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571 TGTATTGTGCTCTCAAGACTTGCCTCAAAATTAACCTGCTGCTGCTGCTGCTGCTG 630
892 ACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 951
631 ATTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 690
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Search completed: January 31, 2004, 02:53:25
Job time : 6766 secs

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Novel human secret
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Human normal uteru
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37 1026.4 56.5 1517 24 AAK12125
38 750 41.3 1839 22 AAD21151
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41 460 25.3 531 22 ABA60454
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ALIGNMENTS

RESULT 1
ID AAF84777 standard; DNA; 1817 BP.
XX AAF84777;
XX AAF84777;
DT 09-JUL-2001 (first entry)
XX Nucleotide sequence of a human chordin-like homologue splice variant.

Splice variant; chordin like homologue; CLH; bone modelling; bone injury;
von-Willebrand factor type C repeat; VWF repeat; bone formation;
reproductive disease; sexual differentiation; miscarriage; tumour;
sexual hormone; cardiovascular disorder; neuronal disease;
neurodegenerative disease; neuron development; ss.
OS Homo sapiens.
XX Key Location/Qualifiers
FH CDS 414..1745
FT /*tag= a
FT /product= "chordin-like homologue splice variant"

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1817	100.0	1817	22 AAF84777	Nucleotide sequenc
2	1772.2	97.5	1890	22 AAF84773	Nucleotide sequenc
3	1417	78.0	1622	22 AAF84778	Nucleotide sequenc
4	1344.4	74.0	1722	22 AAF84775	Nucleotide sequenc
5	1344.4	74.0	1792	22 AAS03538	CDNA encoding Nove
6	1342.8	73.9	1720	22 AAC84305	Human EXCS encodin
7	1342.8	73.9	1731	22 AAS46065	Human DNA encodin
8	1342.8	73.9	1732	21 AAA37064	Human PRO1557 (UNQ

GenCore version 5.1.6
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4 nucleic - nucleic search, using sw model

in on: January 30, 2004, 22:55:38 ; Search time 506 Seconds
(without alignments)
9693.437 Million cell updates/sec

File: US-09-890-456-8

Perfect score: 1817

Sequence: 1 ggacaataaaaggaaaca.....aagttgcataaacatcaaaa 1817

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Archived: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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KX (COMP-) COMPUGEN LTD.
PA Toporok A, Biton S, Savitzky K, Bernatein J;
CX WPI: 2001-308783/32.
DR P-PSDB; AAB68080.
CX Nucleic acids encoding splice variants of a chordin like homolog,
PT useful in the treatment of bone injuries, diseases involved with the
PT female reproductive tract, diseases involving sexual hormone
PT abnormalities and cardiovascular disorders -
CX Claim 1; Page 182-183; 203pp; English.
CX The present sequence encodes a splice variant of a chordin like
CX homologue (CH). The protein is a homologue to the known chordin
CX the von-Willebrand factor type C (VWF) domain repeat, which is found 2-4
CX times in these multi-domain proteins. CLH proteins and polynucleotides
CX can be used for the treatment of diseases which can be ameliorated, cured
CX or prevented by raising the level of a CH. The nucleic acids, expression
CX vectors, proteins and antibodies are useful in the treatment of a disease
CX selected from diseases manifested in non-normal bone formation and
CX non-normal bone modelling, bone injuries, diseases involved with the
CX female reproductive tract, diseases of disorders involved with abnormal
CX sexual differentiation, recurrent miscarriages, tumors of the uterus,
CX breast or prostate, diseases involving sexual hormone abnormalities,
CX cardiovascular disorders, neuronal diseases of the CNS (central nervous
CX system), or neurodegenerative diseases and diseases involving non-normal
CX developments of neurons.
KX
3Q Sequence 1817 BP; 442 A; 534 C; 478 G; 363 T; 0 other;
Query Match 100.0%; Score 1817; DB 22; Length 1817;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1817; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GGACAAATATAAAGGAAACAAAGCATGATTTGAGGCGACAGGAGCGTGGAGCTGAGTCAG 60
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X	09-JUL-2001 (first entry)		
T	Nucleotide sequence of a human chordin-like homologue splice variant.		
E	Splice variant; chordin like homologue; CLH; bone modelling; bone injury;		
X	von-Willebrand factor type C repeat; WFPC repeat; bone formation;		
X	reproductive disease; sexual differentiation; miscarriage; tumour;		
X	sexual hormone; cardiovascular disorder; neuronal disease;		
X	neurodegenerative disease; neuron development; ss.		
S	Homo sapiens.		
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R	28-DEC-1999; 99IL-0133767.		
A	(COMP-) COMPUGEN LTD.		
X	Toporoik A, Biton S, Savitzky K, Bernstein J;		
I	WPI; 2001-308783/32.		
R	P-PADB; AAB68076.		
X	Nucleic acids encoding splice variants of a chordin like homolog,		
T	useful in the treatment of bone injuries, diseases involved with the		
T	female reproductive tract, diseases involving sexual hormone		
T	abnormalities and cardiovascular disorders -		
X	Claim 1; Page 180; 203pp; English.		
X	The present sequence encodes a splice variant of a chordin like		
C	homologue (CLH). The protein is a homologue to the known chordins within		
C	the von-Willebrand factor type C (WFPC) domain repeat, which is found 2-4		
C	times in these multi-domain proteins. The present protein contains 3		
C	WFPC repeats. CLH proteins and polynucleotides can be used for the		
C	treatment of diseases which can be ameliorated, cured or prevented by		
C	raising the level of a CLH. The nucleic acids, expression vectors,		
C	proteins and antibodies are useful in the treatment of a disease selected		
C	from diseases manifested in non-normal bone formation and non-normal bone		

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RESULT 3
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ID AAF84778 standard; DNA; 1622 BP.
XX
AC AAF84778;
XX
DT 09-JUL-2001 (first entry)

XX	Nucleotide sequence of a human chordin-like homologue splice variant.
DE	
XX	Splice variant; chordin like homologue; CLH; bone modelling; bone injury;
XX	von-Willebrand factor type C repeat; VWFC repeat; bone formation;
KW	reproductive disease; sexual differentiation; miscarriage; tumour;
KW	sexual hormone; cardiovascular disorder; neuronal disease;
KW	neurodegenerative disease; neuron development; ss.
XX	
OS	Homo sapiens.
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XX	Key Location/Qualifiers
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XX	WO200134796-A1.
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XX	28-DEC-1999; 99IL-0133767.
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XX	(COMP-) COMPUGEN LTD.
PA	
XX	
XX	Toporoik A, Biton S, Savitzky K, Bernstein J;
PI	
XX	
XX	WPI; 2001-308783/32.
DR	
DR	P-PSDB; AAB68081.
XX	
XX	Nucleic acids encoding splice variants of a chordin like homolog,
PT	useful in the treatment of bone injuries, diseases involved with the
PT	female reproductive tract, diseases involving sexual hormone
PT	abnormalities and cardiovascular disorders -
XX	
XX	Claim 1; Page 183; 203pp; English.
PS	
XX	
CC	The present sequence encodes a splice variant of a chordin like
CC	homologue (CLH). The protein is a homologue to the known chordins within
CC	the von-Willebrand factor type C (VWFC) domain repeat, which is found 2-4
CC	times in these multi-domain proteins. The present protein contains 2
CC	VWFC repeats. CLH proteins and polynucleotides can be used for the
CC	treatment of diseases which can be ameliorated, cured or prevented by
CC	raising the level of a CLH. The nucleic acids, expression vectors,
CC	proteins and antibodies are useful in the treatment of a disease selected
CC	from diseases manifested in non-normal bone formation and non-normal bone
CC	modelling, bone injuries, diseases involved with the female reproductive
CC	tract, diseases of disorders involved with abnormal sexual
CC	differentiation, recurrent miscarriages, tumours of the uterus, breast.
CC	or prostate, diseases involving sexual hormone abnormalities,
CC	cardiovascular disorders, neuronal diseases of the CNS (central nervous
CC	system), or neurodegenerative diseases and diseases involving non-normal
CC	developments of neurons.
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1441 TGCCTGCTTTGCCCTTGGAAACACGAGGCTCGGACTTGGTGGAGATCTACCTCTGGAAGC 1500
1246 TGCCTGCTTTGCCCTTGGAAACACGAGGCTCGGACTTGGTGGAGATCTACCTCTGGAAGC 1305
1501 TGGTAAAGATGAGAAACTGAGGCTCAGAGGTGAAAGTACCTGGCCCAAGGCCACACA 1560
1306 TGGTAAAGATGAGAAACTGAGGCTCAGAGGTGAAAGTACCTGGCCCAAGGCCACACA 1365
1561 GCCAGATCTTCCACTTGACTCAGATCAAGAAAGTCAGAAAGTCAGAAAGTCAGAAAGAG 1620
1366 GCCAGATCTTCCACTTGACTCAGATCAAGAAAGTCAGAAAGTCAGAAAGTCAGAAAGAG 1425
1621 GCACAGCACTTCCGACTGCTCGTGGCCGCCAGAGGTCACTGGAAACGCTTCTCTAGCC 1680
1426 GCACAGCACTTCCGACTGCTCGTGGCCGCCAGAGGTCACTGGAAACGCTTCTCTAGCC 1485
1681 CAGACCTCGAGCTGAAAGTCACGCCCGAGTCCAGACAAAGTGCACCAAGACATAACAAAGA 1740
1486 CAGACCTCGAGCTGAAAGTCACGCCCGAGTCCAGACAAAGTGCACCAAGACATAACAAAGA 1545
1741 CCTAACAGTTCAGATGAGCTGATATTTGTTTATATATATATATATATATATATATATAGAG 1800
1546 CCTAACAGTTCAGATGAGCTGATATTTGTTTATATATATATATATATATATATATATAGAG 1605
1801 TTGCATAACCATCAAAA 1817
1606 TTGCATAACCATCAAAA 1622

RESULT 4
AAF84775
ID AAF84775 standard; DNA; 1722 BP.
XX
AC AAF84775;
XX
DT 09-JUL-2001 (first entry)
XX
DE Nucleotide sequence of a human chordin-like homologue splice variant.
XX
KW Splice variant; chordin like homologue; CLK; bone modelling; bone injury;
KW von-Willebrand factor type C repeat; VWFC repeat; bone formation;
KW reproductive disease; sexual differentiation; miscarriage; tumour;
KW sexual hormone; cardiovascular disorder; neuronal disease;
KW neurodegenerative disease; neuron development; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1650
FT /tag= a
FT /product= "chordin-like homologue splice variant"
XX
FN WO200134796-A1.
XX
PD 17-MAY-2001.
XX
PF 10-NOV-2000; 2000WO-IL00736.
XX
PR 10-NOV-1999; 99IL-0132846.
PR 28-DEC-1999; 99IL-0133767.
XX

181 ATCTGTACAGATTCTACTGTTGATTCCCTAACTGCCCTGTGAGATAGCGTTAAGGCT 240
181 ATCTGTACAGATTCTACTGTTGATTCCCTAACTGCCCTGTGAGATAGCGTTAAGGCT 240
241 CAGACAGTGGCATGCCCCAGTGTGCAAGTAAGTGTGTGTAAGCGAGATCAAAAC 300
241 CAGACAGTGGCATGCCCCAGTGTGCAAGTAAGTGTGTGTAAGCGAGATCAAAAC 300
301 TCAGACCTTCTGGCCCCCTTGCCTAGGAGAGCATGCCAGTTGCTTAGCAGATCTCTTTT 360
301 TCAGACCTTCTGGCCCCCTTGCCTAGGAGAGCATGCCAGTTGCTTAGCAGATCTCTTTT 360
361 GCCTGAGTGGCCAGATGACATCTCTTTAGAGCTAGAAAGAGAGAAATGAGACAGG 420
361 GCCTGAGTGGCCAGATGACATCTCTTTAGAGCTAGAAAGAGAGAAATGAGACAGG 420
421 TCTTTGGGCTGGAGCTCTCTGGGACTACATGGCACTGGTCTGCTTGGCCAGGCCACAGA 480
421 TCTTTGGGCTGGAGCTCTCTGGGACTACATGGCACTGGTCTGCTTGGCCAGGCCACAGA 480
481 TGTCTGCCCTTTCCATGGGAAGAGATCTCCCGGGGAGAGCTGGCACCCCTACTTGG 540
481 TGTCTGCCCTTTCCATGGGAAGAGATCTCCCGGGGAGAGCTGGCACCCCTACTTGG 540
541 AGCCACAGGCTGATGTAAGTCTGCTGCTGCTGTAAGTCTGTAAGGCGGCCATGAGTT 600
541 AGCCACAGGCTGATGTAAGTCTGCTGCTGCTGTAAGTCTGTAAGGCGGCCATGAGTT 600
601 GTTACCGCTCCACTGCTCCGCTGTCACCTGCCCGGAGAGCTGGCAAGTCTGCTTCC 660
601 GTTACCGCTCCACTGCTCCGCTGTCACCTGCCCGGAGAGCTGGCAAGTCTGCTTCC 660
661 GCTGTCCCAAGTGTGGAACCTCAGCTCCCTCTGGACTCCGGGCCCCCAGCAAGTCTCT 720
661 GCTGTCCCAAGTGTGGAACCTCAGCTCCCTCTGGACTCCGGGCCCCCAGCAAGTCTCT 720
721 GCCAGCACAACGGGACCATGTACCAACCGGAGAGATCTTCAAGTGGCCCATGAGCTTCC 780
721 GCCAGCACAACGGGACCATGTACCAACCGGAGAGATCTTCAAGTGGCCCATGAGCTTCC 780
781 CTTCCCGCTGCCCAACAGTGTGCTCTGAGTGTGCAAGGCGCCAGATCTACTGCG 840
781 CTTCCCGCTGCCCAACAGTGTGCTCTGAGTGTGCAAGGCGCCAGATCTACTGCG 840
841 GCCTCACAACCTGCCCGGAGACAGGCTGCCAGCACCCCTCCCGCTGCCAGACTCCTGCT 900
841 GCCTCACAACCTGCCCGGAGACAGGCTGCCAGCACCCCTCCCGCTGCCAGACTCCTGCT 900
901 GCCAAGCTGCARAAGATGAGGCAAGTGCATCGATCGATGAAGGAGACAGTGTGCACTCGC 960
901 GCCAAGCTGCARAAGATGAGGCAAGTGCATCGATCGATGAAGGAGACAGTGTGCACTCGC 960
961 TCCATGGGCTGAGACATCTCAGGATCCATGTTCCAGTGTGTTGGGAGAAAGAGAGGCC 1020
961 TCCATGGGCTGAGACATCTCAGGATCCATGTTCCAGTGTGTTGGGAGAAAGAGAGGCC 1020
1021 CGGCAACCCAGCCCCCTCTGAGCTCAGCGCCCCCTCTGAGCTTCACTCCCTGCGCACTCA 1080
1021 CGGCAACCCAGCCCCCTCTGAGCTCAGCGCCCCCTCTGAGCTTCACTCCCTGCGCACTCA 1080
1081 GACCCAGGGAGGAGGAGAGCACTGTCAGATGCTGTAAGGAGAAACATAGAAG 1140
1081 GACCCAGGGAGGAGGAGAGCACTGTCAGATGCTGTAAGGAGAAACATAGAAG 1140
1141 CCTGTGTGATGGCGGGAAGAGCTACTCCACGGGGAGTGTGGCACCCCGCTTCCGTG 1200
1139 -----
1201 CTTTCGGCCCCCTTGCCCTGCATCTCTATGACCTGTGAGGATGCGCCGAGGACTGCCAGC 1260
1139 -----
1138

(COMP-) COMPUGEN LTD.

Toporoik A, Biton S, Savitzky K, Bernstein J;
WPI: 2001-308783/32.
P-PSDB; AN568078.

Nucleic acids encoding splice variants of a chordin like homolog, useful in the treatment of bone injuries, diseases involved with the female reproductive tract, diseases involving sexual hormone abnormalities and cardiovascular disorders -

Claim 1; Page 181; 203pp; English.

The present sequence encodes a splice variant of a chordin like homologue (CLH). The protein is a homologue to the known chordin within the von-Willebrand factor type C (WFPC) domain repeat, which is found 2-4 times in these multi-domain proteins. The present protein contains 3 WFPC repeats. CLH proteins and polynucleotides can be used for the treatment of diseases which can be ameliorated, cured or prevented by raising the level of a CLH. The nucleic acids, expression vectors, proteins and antibodies are useful in the treatment of a disease selected from diseases manifested in non-normal bone formation and non-normal bone modelling, bone injuries, diseases involved with the female reproductive tract, diseases of disorders involved with abnormal sexual differentiation, recurrent miscarriages, tumours of the uterus, breast or prostate, diseases involving sexual hormone abnormalities, cardiovascular disorders, neuronal diseases of the CNS (central nervous system), or neurodegenerative diseases and diseases involving non-normal developments of neurons.

Sequence 1722 BP; 351 A; 592 C; 426 G; 353 T; 0 other;

Query Match	74.0%	Score 1344.4	DB 22	Length 1722
Best Local Similarity	97.8%	Pred. No. 0		
Matches 1363	Conservative 0	Mismatches 31	Indels 0	Gaps 0
QY	424	TTGGGCTGGAGCCTCTCTGGGACTAA	CATGSCACTGGTCGGTTTGCCAGGCGCCAGACATGT	483
DB	329	TGGGACTCGCGCTGCTCTGTGTTCCCTCTGACTCCCA	CGCTCGAGCCGCGCCAGACATGT	388
QY	484	TCTGCCTTTTCCATGGGAAGAGATACTCC	CCCGCGAGAGCTGSCACCCCTACTTTGGAGC	543
DB	389	TCTGSCCTTTTCCATGGGAAGAGATACTCC	CCCGCGAGAGCTGSCACCCCTACTTTGGAGC	448
QY	544	CACAAGGCCTGATGTACTGCTCGGCTGTACCTGTCT	CAGAGGGCGCCACTGTGAGTTGTT	603
DB	449	CACAAGGCCTGATGTACTGCTCGGCTGTACTCTCT	CAGAGGGCGCCACTGTGAGTTGTT	508
QY	604	ACGCGCTTCCACTGTCCGCCTGTCCACTGCCCC	CGACGCTGTGACGGAGCCACAGCAATGCT	663
DB	509	ACGCGCTTCCACTGTCCGCCTGTCCACTGCCCC	CGACGCTGTGACGGAGCCACAGCAATGCT	568
QY	664	GTCCCAAGTGTGTGGAACTTCCACTCCCTCTGG	AACTCCGGGCCCCACAAAGTCTCTGCC	723
DB	569	GTCCCAAGTGTGTGGAACTTCCACTCCCTCTGG	AACTCCGGGCCCCACAAAGTCTCTGCC	628
QY	724	AGCACACGGGACCATGTACCAACACGGAGAGAT	TCTTCAGTGGCCCATGAGTGTTCCGCT	783
DB	629	AGCACACGGGACCATGTACCAACACGGAGAGAT	TCTTCAGTGGCCCATGAGTGTTCCGCT	688
QY	784	CCGCGCTGCCCAACAGATGTGTCTCTGACAGT	GACAGAGGGCCAGTCTACTTGGCGCC	843
DB	689	CCGCGCTGCCCAACAGATGTGTCTCTGACAGT	GACAGAGGGCCAGTCTACTTGGCGCC	748
QY	844	TCACAACTTGCCCCGAAACCGCTGCCAGAC	CCCCCTCCCGCTGCCAGACTCTGCTGCC	903
DB	749	TCACAACTTGCCCCGAAACCGCTGCCAGAC	CCCCCTCCCGCTGCCAGACTCTGCTGCC	808
QY	904	AAGCCTGCAAGATGACGACGATGAGCAATCG	GATGAGAGGACAGTGTGCACTCGCTCC	963
DB	809	AGGCGCTGCAAGATGAGCAATGAGCAATCG	GATGAGAGGACAGTGTGCACTCGCTCC	868

infectious disease; gene therapy; ss.

Homo sapiens.

Key Location/Qualifiers
3'UTR 1..360
/*tag= a
CDS 361..1717
/*tag= b
5'UTR 1718..1792
/*tag= c

MO200129084-A2.
26-APR-2001.
18-OCT-2000; 2000WO-US28803.
18-OCT-1999; 99US-0160106.
29-OCT-1999; 99US-0162547.
(LEXI-) LEXICON GENETICS INC.
Turner CA, Donoho G, Nehls M, Hilburn E, Zambrowicz B, Sands AT;
WPI; 2001-290898/30.
P-FSDB; AAU02749.

Nucleic acids encoding novel human proteins (NHP), useful for treating physiological or behavioural disorders, cancers and infectious diseases

Disclosure; Page 61; 63pp; English.

The sequence represents the coding sequence of a novel human protein, NHP #1, including open reading frame (ORF) and flanking sequences, isolated from a human adrenal gland cDNA library. NHP nucleotides are useful for drug screening and clinical trial monitoring, and for the diagnosis and treatment of physiological or behavioural disorders, cancer and infectious disease. Nucleotide constructs encoding functional NHPs, mutant NHPs, as well as antisense and ribozyme molecules can also be used in gene therapy for the modulation of NHP expression. NHP polypeptides may be used to produce agonists, antagonists and antibodies for the regulation of NHP expression in the treatment and/or diagnosis of disease.

Sequence 1792 BP; 356 A; 626 C; 439 G; 371 T; 0 other;

Query Match 74.0%; Score 1344.4; DB 22; Length 1792;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1363; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

424 TTGGGCTGGAGCCCTCGGACTAAACATGGCACTGTTCGGTTTGCAGGCCCGCCAGACATGT 483
396 TGGGACTCGCGCTGTCTGTGTTCCCGCTGGACTCCACGCTCGAGCGCGCCAGACATGT 455
484 TCCTCCCTTTCCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCCTACTTGAGC 543
456 CTCGCTTTTTCCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCCTACTTGAGC 515
544 CACAAGGCCCTCATGTACTGCTCGCTGTACCTGTCTCAGAGGGCGCCCATGTGAGTTGTT 603
516 CACAAGGCCCTCATGTACTGCTCGCTGTACCTGTCTCAGAGGGCGCCCATGTGAGTTGTT 575
604 ACCGCTCCCACTGTCCGCTGTGCCACTGCCCCAGCCTGTGACGGAGCCACCAAGAATGCT 663
576 ACCGCTCCCACTGTCCGCTGTGCCACTGCCCCAGCCTGTGACGGAGCCACCAAGAATGCT 635
664 GTCCCAAGTGTGGAACTCACACTCCCTCTGGACTCCGGGGCCCAACAAAGTCCTGCC 723
636 GTCCCAAGTGTGGAACTCACACTCCCTCTGGACTCCGGGGCCCAACAAAGTCCTGCC 695

Db 1776 CATTACCCTCAAAA 1789

RESULT 6
AAC84305
ID AAC84305 standard; cDNA; 1720 BP.
XX
XX AAC84305;
XX
XX 19-MAR-2001 (first entry)
XX
XX Human EXCS encoding cDNA (clone ID 2267403CB1).
XX
XX Extracellular signaling molecule; EXCS; anti-inflammatory; human;
XX KW immunosuppressive; cytostatic; neuroprotective; gastrointestinal;
XX KW viricide; antibacterial; anti-HIV; human immunodeficiency virus;
XX KW antinfertility; cerebroprotective; nootropic; antilicer; antifungal;
XX KW anticonvulsant; tranquilizer; neuroleptic; vasotropic; gynecological;
XX KW keratolytic; protozoacide; gene therapy; ss.
XX
XX Homo sapiens.
OS
XX WO200070049-A2.
XX
XX 23-NOV-2000.
XX
XX 19-MAY-2000; 2000WO-US13975.
XX
XX 19-MAY-1999; 99US-0134949.
XX PR 15-JUL-1999; 99US-0144270.
XX PR 30-JUL-1999; 99US-0146700.
XX PR 04-OCT-1999; 99US-0157508.
XX
XX (INCYTE GENOMICS INC.
PA
XX
XX Tang YT, Yue H, Lal P, Burford N, Bandman O, Baughn MR;
XX PI Azimzai Y, Lu DAM, Patterson C;
PI
XX
XX WPI; 2001-0250321/03.
XX
XX P-PSDB; AAB48069.
XX
XX New human extracellular signaling nucleic acids and polypeptides useful
XX PT for diagnosing, treating and preventing infections and
XX PT gastrointestinal, neurological, reproductive, and
XX PT autoimmune/inflammatory disorders -
XX
XX Claim 4; Page 105-106; 114pp; English.
XX
XX The invention provides human extracellular signaling molecules (EXCS)
XX CC and polynucleotides which identify and encode EXCS. EXCS can be
XX CC expressed by standard recombinant methodology. The amino acid and nucleic
XX CC acid sequences of EXCS are useful for diagnosing, treating and
XX CC preventing infections and gastrointestinal (peptic ulcer, dysphagia,
XX CC pancreatitis), neurological (e.g. epilepsy, ischemic cerebrovascular
XX CC disease, stroke), reproductive (infertility, ovulatory defects,
XX CC endometriosis), autoimmune/inflammatory (actinic keratosis, acquired
XX CC immunodeficiency syndrome (AIDS), Addison's disease), and cell
XX CC proliferative disorders including cancers (of the breast, adrenal gland,
XX CC bone). They may also be used to treat fatal familial insomnia, a
XX CC nutritional and metabolic diseases of the nervous system, myopathies,
XX CC mental disorders (anxiety, schizophrenia, mood), as well as infections
XX CC caused by parasites (malaria, leishmania, trypanosoma), viral
XX CC (adenovirus, coronavirus, flavivirus), bacterial (e.g. pneumococcus,
XX CC staphylococcus, bacillus), and fungal (aspergillus, blastomycetes,
XX CC dermatophytes) agents. The nucleic acids, polypeptides, antagonists,
XX CC agonists, pharmaceutical compositions, and antibodies may also be used
XX CC for treating or preventing disorders associated with increased or
XX CC decreased expression or activity of EXCS. EXCS polynucleotides may also
XX CC be used to detect and quantify gene expression in biopsied tissues in
XX CC which expression of EXCS may be correlated with the disease, to determine
XX CC presence or excess expression of EXCS, to monitor regulation of EXCS
XX CC levels during therapeutic intervention, to detect the presence of

18-SEP-1998; 98US-0101014.
18-SEP-1998; 98US-0101068.
18-SEP-1998; 98US-0101071.
22-SEP-1998; 98US-0101279.
23-SEP-1998; 98US-0101471.
23-SEP-1998; 98US-0101472.
23-SEP-1998; 98US-0101474.
23-SEP-1998; 98US-0101475.
23-SEP-1998; 98US-0101476.
23-SEP-1998; 98US-0101477.
23-SEP-1998; 98US-0101479.
24-SEP-1998; 98US-0101738.
24-SEP-1998; 98US-0101741.
24-SEP-1998; 98US-0101743.
24-SEP-1998; 98US-0101915.
24-SEP-1998; 98US-0101916.
29-SEP-1998; 98US-0102207.
29-SEP-1998; 98US-0102240.
29-SEP-1998; 98US-0102307.
29-SEP-1998; 98US-0102330.
29-SEP-1998; 98US-0102331.
30-SEP-1998; 98US-0102484.
30-SEP-1998; 98US-0102487.
30-SEP-1998; 98US-0102570.
30-SEP-1998; 98US-0102571.
01-OCT-1998; 98US-0102684.
01-OCT-1998; 98US-0102687.
02-OCT-1998; 98US-0102965.
06-OCT-1998; 98US-0103258.
06-OCT-1998; 98US-0103449.
07-OCT-1998; 98US-0103314.
07-OCT-1998; 98US-0103315.
07-OCT-1998; 98US-0103328.
07-OCT-1998; 98US-0103395.
07-OCT-1998; 98US-0103396.
07-OCT-1998; 98US-0103401.
08-OCT-1998; 98US-0103633.
08-OCT-1998; 98US-0103678.
08-OCT-1998; 98US-0103679.
08-OCT-1998; 98US-0103711.
14-OCT-1998; 98US-0104257.
20-OCT-1998; 98US-0104987.
20-OCT-1998; 98US-0105000.
20-OCT-1998; 98US-0105104.
21-OCT-1998; 98US-0105002.
22-OCT-1998; 98US-0105169.
22-OCT-1998; 98US-0105266.
26-OCT-1998; 98US-0105693.
26-OCT-1998; 98US-0105694.
27-OCT-1998; 98US-0105807.
27-OCT-1998; 98US-0105881.
27-OCT-1998; 98US-0105882.
27-OCT-1998; 98US-0106062.
28-OCT-1998; 98US-0106023.
28-OCT-1998; 98US-0106029.
28-OCT-1998; 98US-0106030.
28-OCT-1998; 98US-0106032.
28-OCT-1998; 98US-0106033.
28-OCT-1998; 98US-0106178.
29-OCT-1998; 98US-0106248.
29-OCT-1998; 98US-0106384.
29-OCT-1998; 98US-0108500.
30-OCT-1998; 98US-0106464.
03-NOV-1998; 98US-0106856.
03-NOV-1998; 98US-0106902.
03-NOV-1998; 98US-0106905.
03-NOV-1998; 98US-0106919.
03-NOV-1998; 98US-0106932.
03-NOV-1998; 98US-0106934.
10-NOV-1998; 98US-0107783.
17-NOV-1998; 98US-0108775.
17-NOV-1998; 98US-0108779.
17-NOV-1998; 98US-0108787.
17-NOV-1998; 98US-0108788.
17-NOV-1998; 98US-0108801.
17-NOV-1998; 98US-0108802.
17-NOV-1998; 98US-0108806.
17-NOV-1998; 98US-0108807.
17-NOV-1998; 98US-0108867.
17-NOV-1998; 98US-0108925.
18-NOV-1998; 98US-0108848.
18-NOV-1998; 98US-0108849.
18-NOV-1998; 98US-0108850.
18-NOV-1998; 98US-0108851.
18-NOV-1998; 98US-0108852.
18-NOV-1998; 98US-0108858.
18-NOV-1998; 98US-0108904.
PA (GETH) GENENTECH INC.
XX
XX Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
PI
XX
XX WPI; 2000-237871/20.
DR P-PSDB; AAY99382.
XX
XX New mammalian DNA sequences encoding transmembrane, receptor or
PT secreted PRO polypeptides, useful for screening of potential peptide or
PT small molecule inhibitors of the relevant receptor/ligand interactions
XX
XX Claim 2; Fig 85; 773pp; English.
XX
XX AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
CC transmembrane and receptor PRO proteins can be used for screening of
CC potential peptide or small molecule inhibitors of the relevant
CC receptor/ligand interactions. The polypeptides and nucleotide sequences
CC encoding then have various industrial applications, including uses as
CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent
CC PCR primers and hybridisation probes used in the isolation of the PRO
CC polypeptides from the present invention.
XX
SQ Sequence 1732 BP; 369 A; 592 C; 425 G; 346 T; 0 other;
Query Match 73.9%; Score 1342.8; DB 21; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 424 TTGGCTGGAGCTCTCGGACTAACATGGCACTGGTGGTTCGCCAGGCGCCAGACATGT 483
DB 321 TGGACTCGGCTGCTCTGGTTCCTGGACTCCACGCTCGAGCGCGCCAGACATGT 380
QY 484 TCTGCTTTTCCATGGGAAGAGATATCTCCCGGGAGAGCTGGCACCCCTACTTGGAGC 543
DB 381 TCTGCTTTTCCATGGGAAGAGATATCTCCCGGGAGAGCTGGCACCCCTACTTGGAGC 440
QY 544 CACAAGGCTGATGTACTGCTGCGCTGTACTGCTCAGAGGGGCGCCATGTGAGTTGTT 603
DB 441 CACAAGGCTGATGTACTGCTGCGCTGTACTGCTCAGAGGGGCGCCATGTGAGTTGTT 500
QY 604 ACCGCTCCACTGTCCGCTCTCCACTGCCCGCCAGCTGTGAGGGAGCCACCAATGCT 663
DB 501 ACCGCTCCACTGTCCGCTCTCCACTGCCCGCCAGCTGTGAGGGAGCCACCAATGCT 560
QY 664 GTCCAAAGTGTGGAACTCACACTCCCTCTGGACTCCGCGCCGCCCAAGTCTGTC 723
DB 561 GTCCAAAGTGTGGAACTCACACTCCCTCTGGACTCCGCGCCGCCCAAGTCTGTC 620
QY 724 AGCAACGGGACCATGTACCAACCGGAGAGATTTAGTGCCTCCATGAGCTTTCCCT 783
DB 621 AGCAACGGGACCATGTACCAACCGGAGAGATTTAGTGCCTCCATGAGCTTTCCCT 680
QY 784 CCGGCTGCCCAACCATGTGCTCTGAGTGCACAGAGGGCCAGATCTACTGGGCC 843
DB 681 CCGGCTGCCCAACCATGTGCTCTGAGTGCACAGAGGGCCAGATCTACTGGGCC 740
QY 844 TCACAACCTGCCCGGACCAAGGCTGCCAGGACCCCTCCCGCTGCCAGACTCTCTGCTGCC 903

Db	741	TCACAACTGCCCCGAGACACGAGTGGCCAGCACCCCTCCCACTGCCAGACTCTCTGTGTC	800
Qy	904	AAGCCTGAAAGATGAGGCAAGTGAAGATCGAATCGAATGAAGAGCAGTGTGAGTGTGCTCC	963
Db	801	AAGCCTGAAAGATGAGGCAAGTGAAGATCGAATCGAATGAAGAGCAGTGTGAGTGTGCTCC	860
Qy	964	ATGGGCTGAGACATCTCAGGATCCATGTTCCAGTGTGAGGAGAAAGAGAGGCGCGG	1023
Db	861	ATGGGCTGAGACATCTCAGGATCCATGTTCCAGTGTGAGGAGAAAGAGAGGCGCGG	920
Qy	1024	GCACCCGAGCCCGCACTGGCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC	1083
Db	921	GCACCCGAGCCCGCACTGGCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC	980
Qy	1084	CAAAGGAGAGGAGAGCAACAATGTCAAGATCTCTGAGGAGAAACATAAAGAAAGCCT	1143
Db	981	CAAAGGAGAGGAGAGCAACAATGTCAAGATCTCTGAGGAGAAACATAAAGAAAGCCT	1040
Qy	1144	GTGTCATGGCGGGAAGACGTACTCTCCACGGGAGGTGTGGCACCCTCCGTCGCT	1203
Db	1041	GTGTCATGGCGGGAAGACGTACTCTCCACGGGAGGTGTGGCACCCTCCGTCGCT	1100
Qy	1204	TGGGCTTGTGCTGCTGATCTGATGACCTGTGAGGATGCGCGCAGGACTGCCAGCGTG	1263
Db	1101	TGGGCTTGTGCTGCTGATCTGATGACCTGTGAGGATGCGCGCAGGACTGCCAGCGTG	1160
Qy	1264	TGACCTGTCCCAACGAGTACCCCTGCGCTGACCCGAGAAAGTGGCTGGGAAGTGTGCA	1323
Db	1161	TGACCTGTCCCAACGAGTACCCCTGCGCTGACCCGAGAAAGTGGCTGGGAAGTGTGCA	1220
Qy	1324	AGATTGCGCAGAGGAAAGAGAGACCTTGGCCACAGTGAATCAGTGTACCAAGGTGTC	1383
Db	1221	AGATTGCGCAGAGGAAAGAGAGACCTTGGCCACAGTGAATCAGTGTACCAAGGTGTC	1280
Qy	1384	CAAAGGACCGGCGCGGCTCTGTCACACATCGGTATCCCAAGCCAGACACCTGC	1443
Db	1281	CAAAGGACCGGCGCGGCTCTGTCACACATCGGTATCCCAAGCCAGACACCTGC	1340
Qy	1444	GTCGCTTTGCTTGGACAGGAGGCTCGGACTTGTGGAGATCTACTCTGGAAGCTGG	1503
Db	1341	GTCGCTTTGCTTGGACAGGAGGCTCGGACTTGTGGAGATCTACTCTGGAAGCTGG	1400
Qy	1504	TAAAGATGAGGAAATGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCC	1563
Db	1401	TAAAGATGAGGAAATGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCC	1460
Qy	1564	AGAATTTCCACTTGACTCAGATCAAGAAAGTCAAGGAGCAAGACTTCCAGAAAGAGGCA	1623
Db	1461	AGAATTTCCACTTGACTCAGATCAAGAAAGTCAAGGAGCAAGACTTCCAGAAAGAGGCA	1520
Qy	1624	CAGCACTTCGAGTCTGCTGCTGCGCCCGCCAGAGGTCACTGGACGTTCTTCTAGCCAG	1683
Db	1521	CAGCACTTCGAGTCTGCTGCTGCGCCCGCCAGAGGTCACTGGACGTTCTTCTAGCCAG	1580
Qy	1684	ACCTCGAGTGAAGTCAAGGCGAGTCCAGCAAAAGTGAACAGACATAAAGAGCT	1743
Db	1581	ACCTCGAGTGAAGTCAAGGCGAGTCCAGCAAAAGTGAACAGACATAAAGAGCT	1640
Qy	1744	AACAGTTGAGATGATGAGTGTATAATTTGTTTATTATATATATATATATATATATATAT	1803
Db	1641	AACAGTTGAGATGATGAGTGTATAATTTGTTTATTATATATATATATATATATATATAT	1700
Qy	1804	CATAACCATCAAAA	1817
Db	1701	CATTACCTCAAAA	1714

RESULT 9
AAF92098
ID AAF92098 standard; cDNA; 1732 BP.
XX
AC AAF92098;

501 ACCGCTCCACTGTCCGCTGTCCACTGCCCCCGCCCTGTGACGGAGCCACAGCAATGCT 560
564 GTCCCAAGTGTGGAACTTCACTCTGACTCGGCGCCCGCCCAAGTCTCTGCC 723
561 GTCCCAAGTGTGGAACTTCACTCTGACTCGGCGCCCGCCCAAGTCTCTGCC 620
724 AGCACAAGCGGACCATGTACCAACACGAGAGATCTTCAGTGGCCCATGAGCTGTTCCTCT 783
621 AGCACAAGCGGACCATGTACCAACACGAGAGATCTTCAGTGGCCCATGAGCTGTTCCTCT 680
784 CCGCCTTCCCAACACGAGTGTCTCTGAGTGACAGAGGCGCCAGATCTACTGCGGCC 843
681 CCGCCTTCCCAACACGAGTGTCTCTGAGTGACAGAGGCGCCAGATCTACTGCGGCC 740
844 TCACAACCTGCCCGCAACAGGCTGCGCAGACCCCTCCGCTGCGCAGACTCTCTGTCTGCC 903
741 TCACAACCTGCCCGCAACAGGCTGCGCAGACCCCTCCCACTGCCAGACTCTCTGTCTGCC 800
904 AAGCCTTCAAGATGAGCAAGTGAAGCAATCGGATGAAGAGACAGTGTGCACTGCTCTCC 963
801 AAGCCTTCAAGATGAGCAAGTGAAGCAATCGGATGAAGAGACAGTGTGCACTGCTCTCC 860
964 ATGGGGTGAGACATCTCCAGGATCCATCTTCAGTGATGCTGGGAGAAAGAGAGGCGCG 1023
861 ATGGGGTGAGACATCTCCAGGATCCATCTTCAGTGATGCTGGGAGAAAGAGAGGCGCG 920
1024 GCACCCCGACCCCGACCTGCGCTCAGCGCCCTCTGAGCTTTCATCCCTCGCCACTTCAGAC 1083
921 GCACCCCGACCCCGACCTGCGCTCAGCGCCCTCTGAGCTTTCATCCCTCGCCACTTCAGAC 980
1084 CCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1143
981 CCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1040
1144 GTGTGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1203
1041 GTGTGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1100
1204 TCGGCGCCCTTGCCTGATCTATGACCTGTGAGGATGCGCGCAGGAGTGCACGCGTG 1263
1101 TCGGCGCCCTTGCCTGATCTATGACCTGTGAGGATGCGCGCAGGAGTGCACGCGTG 1160
1264 TGACCTTCCCGACGAGTACCCCTGCGCTCAGCCGAGAAAGTGGTGGGAGTGTGCA 1323
1161 TGACCTTCCCGACGAGTACCCCTGCGCTCAGCCGAGAAAGTGGTGGGAGTGTGCA 1220
1324 AGATTGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1383
1221 AGATTGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1280
1384 CCAAGGACCGGGCGGGTCTCTGTCACATCGGTATCCCAAGCCAGACCACTGCG 1443
1281 CCAAGGACCGGGCGGGTCTCTGTCACATCGGTATCCCAAGCCAGACCACTGCG 1340
1444 GTCGCTTTCGCTGGAACACAGGCGCTCGGCTTGTGAGATCTACCTCTGGAAGCTG 1503
1341 GTCGCTTTCGCTGGAACACAGGCGCTCGGCTTGTGAGATCTACCTCTGGAAGCTG 1400
1504 TAAAGATGAGGAACTCAGGCTCAGAGAGTGAAGTACCTCGCCCAAGGCGCACAGCC 1563
1401 TAAAGATGAGGAACTCAGGCTCAGAGAGTGAAGTACCTCGCCCAAGGCGCACAGCC 1460
1564 AGAATCTTCCACTTGAATCAGATCAAGAAAGTCAAGAGCAAGATCTCAGAAAGAGGCA 1623
1461 AGAATCTTCCACTTGAATCAGATCAAGAAAGTCAAGAGCAAGATCTCAGAAAGAGGCA 1520
1624 CAGCACTTCGAGCTGCTCGCTGCGGCGCCCGCCAGAGGCTACTGGAAGCTCTTCTAGCCGAG 1683
1521 CAGCACTTCGAGCTGCTCGCTGCGGCGCCCGCCAGAGGCTACTGGAAGCTCTTCTAGCCGAG 1580
1684 ACCCTGGAGCTGAAGGTCACCGGCGAGTCCAGACAAAGTGACCAAGACATACCAAGACCT 1743
1581 ACCCTGGAGCTGAAGGTCACCGGCGAGTCCAGACAAAGTGACCAAGACATACCAAGACCT 1640

QY 1744 AACAGTTGCAGATGAGCTGTATAATTTGTTTATATATATATATAAATAGAGCTTG 1803
Db 1641 AACAGTTGCAGATGAGCTGTATAATTTGTTTATATATATATATAAATAGAGCTTG 1700
QY 1804 CATAACCATCAAAA 1817
Db 1701 CATTACCTCAAAA 1714
RESULT 10
AAP54300
ID AAP54300 standard; DNA; 1732 BP.
XX AAP54300;
AC AAP54300;
XX XX
DT 02-APR-2001 (first entry)
XX
DE DNA encoding protein of the invention #43.
XX
KW Secreted; transmembrane; gene therapy; ss.
XX
OS Unidentified.
XX
PN WO200078961-A1.
XX
PD 28-DEC-2000.
XX
PF 18-FEB-2000; 2000WO-US04342.
XX
PR 23-JUN-1999; 99US-0141037.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 01-SEP-1999; 99WO-US20111.
PR 29-OCT-1999; 99US-0152506.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28551.
PR 16-DEC-1999; 99WO-US30095.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Geddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D;
PI Watanabe CK, Williams PM, Wood WI;
DR WPI; 2001-071395/08.
XX
PT Secreted and transmembrane proteins and nucleic acids designated PRO.
PT useful as hybridization probes, in chromosome and gene mapping and gene
therapy -
XX
PS Claim 2; Fig 85; 787pp; English.
XX
CC The present invention relates to secreted and transmembrane proteins.
CC These proteins and the DNA encoding them may be used as hybridization
CC probes, in chromosome and gene mapping and in the generation of
CC anti-sense RNA and DNA. They may also be used to generate either
CC transgenic animals or knockout animals which are in turn useful for
CC development and screening of therapeutically useful reagents.
CC The nucleic acids may also be used in gene therapy.
XX
SQ Sequence 1732 BP; 369 A; 592 C; 425 G; 346 T; 0 other;

Query Match 73.9%; Score 1342.8; DB 22; Length 1732;
Best Local Similarity 97.7%; Pred. NO. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 424 TTGGGCTGGAGCCTCTCGGAGTAACTGGGACTCCCGCTGGACTCCCGAGCCGAGACATGT 483
Db 321 TGGGACTCGGCTGCTCTGGTTCCTCCCTGGACTCCCGAGCCGAGACATGT 380

484	49	TC	TCTGCCCTTTTTCATGGGAAGAGATAC	TCCCCCGCGAGAGCTGGCACCCCTACTTTGGAGC	543
381	Db		TCTGCCCTTTTTCATGGGAAGAGATAC	TCCCCCGCGAGAGCTGGCACCCCTACTTTGGAGC	440
544	2y	CACAAGGCCTGATGTA	CTGCTGCGCTGTACCTGTCTCAGAGGGGCCCATGTGAGTTGTTT	603	
441	Db	CACAAGGCCTGATGTA	CTGCTGCGCTGTACCTGTCTCAGAGGGGCCCATGTGAGTTGTTT	500	
604	2y	ACCGCCTTCACTGTG	CCGCTGTCCACTGCGCCCGCAGCTGTGACGGAGCCACAGCAATGCT	663	
501	Db	ACCGCCTTCACTGTG	CCGCTGTCCACTGCGCCCGCAGCTGTGACGGAGCCACAGCAATGCT	560	
664	2y	GTCCCAAGTGTGTGAA	CTCACACTTCCCTCTGGACTCCCGGGGCCCAACCAAGTCTCTGCC	723	
561	Db	GTCCCAAGTGTGTGAA	CTCACACTTCCCTCTGGACTCCCGGGGCCCAACCAAGTCTCTGCC	620	
724	2y	AGCAACAACGGGACCA	TGTAACCAACGGAGAGATCTTCACTGTCCTTCACTGAGTGTTCCT	783	
621	Db	AGCAACAACGGGACCA	TGTAACCAACGGAGAGATCTTCACTGTCCTTCACTGAGTGTTCCT	680	
784	Qy	CCGGCTGCGCCAA	CCAGTGTGTCTCTGAGCTGTGCACAGAGGGCCAGATCTACTTGC	843	
681	Db	CCGGCTGCGCCAA	CCAGTGTGTCTCTGAGCTGTGCACAGAGGGCCAGATCTACTTGC	740	
844	Qy	TCACAACCTGCCCCG	AAACAGGCTGCCACACCCCTCCCGCTCCCGACACTCTCTGCTGCC	903	
741	Db	TCACAACCTGCCCCG	AAACAGGCTGCCACACCCCTCCCGCTCCCGACACTCTCTGCTGCC	800	
904	Qy	AAGCCTGCAAAAGAT	GAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGAGTGCCTCC	963	
801	Db	AAGCCTGCAAAAGAT	GAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGAGTGCCTCC	860	
964	Qy	ATGGGGTGAGACAT	CTCTAGGATCCATGTTCCAGTGATGCTGGAGAAAGAGAGCCCGG	1023	
861	Db	ATGGGGTGAGACAT	CTCTAGGATCCATGTTCCAGTGATGCTGGAGAAAGAGAGCCCGG	920	
1024	Qy	GCACCCGAGCCCCAC	TGSCCTCAGGCCCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC	1083	
921	Db	GCACCCGAGCCCCAC	TGSCCTCAGGCCCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC	980	
1084	Qy	CAAAGGGAGCAGGCA	CAACCTGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCT	1143	
981	Db	CAAAGGGAGCAGGCA	CAACCTGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCT	1040	
1144	Qy	GTGTGCATGGCGGAA	AGACGTATCCACGGGAGGTGTGGCACCCGCGCTTCCGTGCT	1203	
1041	Db	GTGTGCATGGCGGAA	AGACGTATCCACGGGAGGTGTGGCACCCGCGCTTCCGTGCT	1100	
1204	Qy	TCGGCCCCCTTGCTG	ATCCTATGACCTGTGAGGATGGCCGCGAGACTGCCACGCTG	1263	
1101	Db	TCGGCCCCCTTGCTG	ATCCTATGACCTGTGAGGATGGCCGCGAGACTGCCACGCTG	1160	
1264	Qy	TGACCTGTCCACCGA	TACCCCTCGCTCACCCCGAGAAAGTGGCTGGGAAGTGTGCA	1323	
1161	Db	TGACCTGTCCACCGA	TACCCCTCGCTCACCCCGAGAAAGTGGCTGGGAAGTGTGCA	1220	
1324	Qy	AGATTTGCCACAGAG	CAAAAGCAGACCTCGTCCACACAGTGTGATCAGTTCTACAGGTGTC	1383	
1221	Db	AGATTTGCCACAGAG	CAAAAGCAGACCTCGTCCACACAGTGTGATCAGTTCTACAGGTGTC	1280	
1384	Qy	CCAAGGCAACGGGCG	GGTCTCTGTCCACATCGGTATCCCCAAGCCAGACACCTGC	1443	
1281	Db	CCAAGGCAACGGGCG	GGTCTCTGTCCACATCGGTATCCCCAAGCCAGACACCTGC	1340	
1444	Qy	GTGCGCTTTGGCCCT	GTGAACACGAGGCGCTCGGACTTGGTGAGATCTACCTCTGGAAGCTG	1503	
1341	Db	GTGCGCTTTGGCCCT	GTGAACACGAGGCGCTCGGACTTGGTGAGATCTACCTCTGGAAGCTG	1400	
1504	Qy	TAAAAGATGAGGAA	ACTGAGGCTCAGAGAGTGTAAGTACCTTGGCCCAAGGCCACACAGCC	1563	
1401	Db	TAAAAGATGAGGAA	ACTGAGGCTCAGAGAGTGTAAGTACCTTGGCCCAAGGCCACACAGCC	1460	

Qy	1564	AGAACTCTTCCACTTGAGCTCAGATCAAGAAAGTCAGGAGCAAGCAAGACTTCCAGAAAGAGGCA	1622
Db	1461	AGAACTCTTCCACTTGAGCTCAGATCAAGAAAGTCAGGAGCAAGCAAGACTTCCAGAAAGAGGCA	1520
Qy	1624	CAGCACTTCCGACTGCTCGCTGSCCCGCCACGAAAGTCACCTGGAACGCTTCTCTAGCCCCAG	1683
Db	1521	CAGCACTTCCGACTGCTCGCTGSCCCGCCACGAAAGTCACCTGGAACGCTTCTCTAGCCCCAG	1580
Qy	1684	ACCTTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAGACATACAAAGACCT	1743
Db	1581	ACCTTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAGACATACAAAGACCT	1640
Qy	1744	AACAGTTGCAGATATGAGCTGTATATTTGTTTATTATATATTAATTAATAAAGAGTTG	1803
Db	1641	AACAGTTGCAGATATGAGCTGTATATTTGTTTATTATATATTAATTAATAAAGAGTTG	1700
Qy	1804	CATAACCATCAAAA	1817
Db	1701	CATTACCCCTCAAAA	1714
RESULT 11			
ABS74418			
ID	ABS74418 standard; cDNA; 1732 BP.		
XX	ABS74418;		
XX	10-DEC-2002 (first entry)		
XX	Human cDNA encoding secreted/transmembrane protein PRO1557.		
DE	Human; ss; gene; secreted protein; transmembrane protein; antirheumatic;		
KW	antiarthritic; osteopathic; sports-related joint problem;		
KW	articular cartilage defect; osteoarthritis; rheumatoid arthritis.		
XX	Homo sapiens.		
OS	US2002119130-A1.		
XX	29-AUG-2002.		
PD	06-DEC-2001; 2001US-0006867.		
XX	29-OCT-1997; 97US-063435P.		
XX	29-OCT-1997; 97US-064215P.		
PR	22-APR-1998; 98US-082797P.		
PR	29-APR-1998; 98US-083435P.		
PR	15-MAY-1998; 98US-085579P.		
PR	10-JUN-1998; 98US-088811P.		
PR	10-JUN-1998; 98US-088824P.		
PR	10-JUN-1998; 98US-088825P.		
PR	11-JUN-1998; 98US-088863P.		
PR	12-JUN-1998; 98US-089105P.		
PR	16-JUN-1998; 98US-089514P.		
PR	16-SEP-1998; 98WO-US19330.		
PR	08-NAR-1999; 99WO-US05028.		
PR	14-MAY-1999; 99WO-US10733.		
PR	02-JUN-1999; 99WO-US12252.		
PR	01-SEP-1999; 99WO-US20111.		
PR	15-SEP-1999; 99WO-US21090.		
PR	15-SEP-1999; 99WO-US21194.		
PR	22-DEC-1999; 99WO-US30720.		
PR	18-FEB-2000; 2000WO-US04341.		
PR	18-FEB-2000; 2000WO-US04342.		
PR	30-MAR-2000; 2000WO-US08439.		
PR	22-MAY-2000; 2000WO-US14042.		
PR	02-JUN-2000; 2000WO-US15264.		
PR	23-AUG-2000; 2000WO-US23522.		
PR	24-AUG-2000; 2000WO-US23328.		
PR	10-NOV-2000; 2000WO-US30873.		
PR	01-DEC-2000; 2000WO-US32378.		
PR	20-DEC-2000; 2000WO-US34956.		
PR	28-FEB-2001; 2001WO-US06520.		

R 20-JUN-2001; 2001WO-US19692.
R 29-JUN-2001; 2001WO-US21066.
R 09-JUL-2001; 2001WO-US21735.
X (GETH) GENENTECH INC.
X Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
X Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
X WPI: 2002-731348/79.
X P-PSDB; ABG95891.
X
X New isolated secreted and transmembrane PRO polypeptide useful for
X modulating biological activity of a cell, or for treating
X sports-related joint problems, osteoarthritis or rheumatoid arthritis
X
X Claim 2; Fig 81; 399pp; English.
X
X The invention relates to an isolated secreted and transmembrane PRO
X polypeptide having 80 % sequence identity to a sequence appearing
X as ABG95851-ABG95934 or their associated signal peptide, or a sequence of
X an extracellular domain of the proteins with their associated signal
X peptide or lacking its associated signal peptide. Also included are
X the nucleic acids encoding the proteins, vectors, host cells,
X fusion proteins and antibodies which specifically bind to the proteins.
X The proteins are useful for detecting a polypeptide designated as A, B, C
X or D in a sample suspected of containing an A, B, C or D polypeptide,
X by contacting the sample with a polypeptide designated as E, F, G, H or
X I (or vice versa) and determining the formation of an A/E, B/F, G/H
X or D/I polypeptide conjugate in the sample, where the formation of the
X conjugate is indicative of the presence of an A, B, C or D polypeptide
X in the sample, where A is a PRO10272 polypeptide, B is a PRO20110
X polypeptide, C is a PRO10096 polypeptide, D is a PRO19760 polypeptide,
X E is a PRO5801 polypeptide, F is a PRO1 polypeptide, G is a PRO20040
X polypeptide, H is a PRO20233 polypeptide and I is a PRO1890
X polypeptide. The sample comprises a cell suspected of expressing the A,
X B, C or D polypeptide. The E, F, G, H or I polypeptide is labeled with
X a detectable label or is attached to a solid support. The proteins are
X useful for linking a bioactive molecule to a cell expressing a
X polypeptide designated as A, B, C or D or E, F, G, H or I. The bioactive
X molecule is a toxin, a radiolabel or an antibody. The bioactive molecule
X causes death of the cell. A, B, C, D, E, F, G, H, or I, or antibodies
X against them are useful for modulating a biological activity of a cell
X expressing a polypeptide designated as A, B, C or D or E, F, G, H, or
X I. The cell is killed. The proteins are useful for identifying
X agonists or antagonists, for the preparation of a medicament useful in
X the treatment of a condition which is responsive to the proteins, as
X molecular weight markers for protein electrophoresis purposes, and as
X therapeutic agents for treating sports-related joint problems,
X articular cartilage defects, osteoarthritis or rheumatoid arthritis.
X Nucleic acids encoding the proteins are useful as hybridisation probes,
X in chromosome and gene mapping, in the generation of anti-sense RNA and
X DNA, for the preparation of the proteins, to generate transgenic or
X knockout animals which are useful in the development and screening of
X therapeutic useful reagents, for chromosome identification, and in gene
X therapy. The antibody is useful as a therapeutic agent, in a diagnostic
X assay and for affinity purification of the protein from recombinant
X cell culture natural sources. The present invention encodes a novel
X secreted or transmembrane protein of the invention.

Q Sequence 1732 BP; 369 A; 592 C; 425 G; 346 T; 0 other;
Query Match 73.9%; Score 1342.8; DB 24; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
Y 424 TTGGGCTGGAGCTCTCGTGACTAACATGGCACTGGTTCGGTTTGGCAGGCCGAGACATGT 483
b 321 TGGGACTCGGCTGCTCTGTGTTCCCTTGGACTCCACGCTCGAGCCCGCCGAGACATGT 380
Y 484 TTGCGCTTTTCCATGGGAAGAGATACTCCCGCGGAGAGCTGGCACCCCTACTTGGAGC 543
b 381 TCTGCTTTTCCATGGGAAGAGATACTCCCGCGGAGAGCTGGCACCCCTACTTGGAGC 440

QY	544	CACAAGCCCTGATGTACTGCTGCGCTGTACTCTGCTCAGAGGGGCCCCATGTGAGTTGTT	603
DB	441	CACAAGCCCTGATGTACTGCTGCGCTGTACTCTGCTCAGAGGGGCCCCATGTGAGTTGTT	500
QY	604	ACGGCCCTCACTGTCCGCTGTCCACTGCCCCCAGCCCTGTGACGGAGCCACAGCAATGCT	663
DB	501	ACGGCCCTCACTGTCCGCTGTCCACTGCCCCCAGCCCTGTGACGGAGCCACAGCAATGCT	560
QY	664	GTCCCAAGTGTGTGGAACTTCACACTCCCTCTGAGCTCCGGGCCCCACCAAGTCTCTGCC	723
DB	561	GTCCCAAGTGTGTGGAACTTCACACTCCCTCTGAGCTCCGGGCCCCACCAAGTCTCTGCC	620
QY	724	AGCACAAACGGGACCATGTATCAACACACGGAGAGATCTTTCAGTGCCCATGAGTGTTCCT	783
DB	621	AGCACAAACGGGACCATGTATCAACACACGGAGAGATCTTTCAGTGCCCATGAGTGTTCCT	680
QY	784	CCCGCTGCCCCAACCAAGTGTCTCTGCACTGCACAGAGGGCCAGATCTTACTGCGGCC	843
DB	681	CCCGCTGCCCCAACCAAGTGTCTCTGCACTGCACAGAGGGCCAGATCTTACTGCGGCC	740
QY	844	TCACAACCTGCCCCGAAACAGGCTGCCAGACCCCTCCCTGCTGCCAGACTCTCTGCTGCC	903
DB	741	TCACAACCTGCCCCGAAACAGGCTGCCAGACCCCTCCCTGCTGCCAGACTCTCTGCTGCC	800
QY	904	AGCCTGCAAGATGAGGCAAGTGAAGTCAATCGGATGAAGAGACAGTGTGCAAGTCTGCTCC	963
DB	801	AGCCTGCAAGATGAGGCAAGTGAAGTCAATCGGATGAAGAGACAGTGTGCAAGTCTGCTCC	860
QY	964	ATGGGCTGAGACATCTCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGG	1023
DB	861	ATGGGCTGAGACATCTCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGG	920
QY	1024	GCACCCCGAGCCCACTGGCTCAGCCCTCAGCCCTCTGAGCTTATCCCTCGCCACTTCAGAC	1083
DB	921	GCACCCCGAGCCCACTGGCTCAGCCCTCAGCCCTCTGAGCTTATCCCTCGCCACTTCAGAC	980
QY	1084	CAAGGAGCAGCAGCAGCACAACCTGTCAAGATGCTCTGAGGAGAAACATATAAGAGCCT	1143
DB	981	CAAGGAGCAGCAGCAGCACAACCTGTCAAGATGCTCTGAGGAGAAACATATAAGAGCCT	1040
QY	1144	GTGTGATGCGGGAGACAGCTACTCCCAAGGGAGGTGTGCGCCAGCCGCTTCCGTTGCT	1203
DB	1041	GTGTGATGCGGGAGACAGCTACTCCCAAGGGAGGTGTGCGCCAGCCGCTTCCGTTGCT	1100
QY	1204	TCGGCCCTTGGCTGCTATGCTATGACCTGTGAGGATGCGCCAGGAGCTCCAGCGTG	1263
DB	1101	TCGGCCCTTGGCTGCTATGCTATGACCTGTGAGGATGCGCCAGGAGCTCCAGCGTG	1160
QY	1264	TGACCTGTCCACCGAGTACCCCTGCGCTCACCCCGAGAAAGTGGCTGGAAAGTGTGCA	1323
DB	1161	TGACCTGTCCACCGAGTACCCCTGCGCTCACCCCGAGAAAGTGGCTGGAAAGTGTGCA	1220
QY	1324	AGATTTGCCAGAGGACAAAGAGACACCTGCGCCACAGTGAGATCAGTCTACAGGTGTC	1383
DB	1221	AGATTTGCCAGAGGACAAAGAGACACCTGCGCCACAGTGAGATCAGTCTACAGGTGTC	1280
QY	1384	CAAGGACCGCGCGGGTCTCTGTCACACATCGTATCCCAAGCCAGACCAACCTGC	1443
DB	1281	CAAGGACCGCGCGGGTCTCTGTCACACATCGTATCCCAAGCCAGACCAACCTGC	1340
QY	1444	GTGCTTTGGCTGGAAACAGAGGCTTCGGACTTGGTGAGATCTTACCTCTCGAAGCTGG	1503
DB	1341	GTGCTTTGGCTGGAAACAGAGGCTTCGGACTTGGTGAGATCTTACCTCTCGAAGCTGG	1400
QY	1504	TAAAGATGAGGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACAGCC	1563
DB	1401	TAAAGATGAGGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACAGCC	1460
QY	1564	AGAATCTTCCACTTGAATCAGATCAAGAAAGTCAAGAAAGCAAGCTTCCAGAAAGGCA	1623
DB	1461	AGAATCTTCCACTTGAATCAGATCAAGAAAGTCAAGAAAGCAAGCTTCCAGAAAGGCA	1520

PR	29-APR-2001,	2001WO-US27099	PR
PR	18-SEP-1997,	97US-052636P	PR
PR	18-SEP-1997,	97US-059266P	PR
PR	18-SEP-1997,	97US-062250P	PR
PR	17-OCT-1997,	97US-063486P	PR
PR	24-OCT-1997,	97US-063120P	PR
PR	24-OCT-1997,	97US-063121P	PR
PR	28-OCT-1997,	97US-063540P	PR
PR	28-OCT-1997,	97US-063541P	PR
PR	28-OCT-1997,	97US-063544P	PR
PR	28-OCT-1997,	97US-063564P	PR
PR	29-OCT-1997,	97US-063734P	PR
PR	31-OCT-1997,	97US-063870P	PR
PR	31-OCT-1997,	97US-064103P	PR
PR	13-NOV-1997,	97US-065311P	PR
PR	21-NOV-1997,	97US-066120P	PR
PR	24-NOV-1997,	97US-066466P	PR
PR	24-NOV-1997,	97US-066772P	PR
PR	11-DEC-1997,	97US-069335P	PR
PR	12-DEC-1997,	97US-069425P	PR
PR	18-DEC-1997,	97US-069870P	PR
PR	17-DEC-1997,	97US-068017P	PR
PR	10-MAR-1998,	98US-077450P	PR
PR	11-MAR-1998,	98US-077632P	PR
PR	11-MAR-1998,	98US-077643P	PR
PR	20-MAR-1998,	98US-078888P	PR
PR	20-MAR-1998,	98US-078933P	PR
PR	27-MAR-1998,	98US-079664P	PR
PR	27-MAR-1998,	98US-079686P	PR
PR	31-MAR-1998,	98US-080107P	PR
PR	31-MAR-1998,	98US-080119P	PR
PR	01-APR-1998,	98US-080194P	PR
PR	01-APR-1998,	98US-080327P	PR
PR	01-APR-1998,	98US-080333P	PR
PR	08-APR-1998,	98US-081043P	PR
PR	08-APR-1998,	98US-081070P	PR
PR	08-APR-1998,	98US-081195P	PR
PR	15-APR-1998,	98US-081838P	PR
PR	21-APR-1998,	98US-082568P	PR
PR	21-APR-1998,	98US-082569P	PR
PR	22-APR-1998,	98US-082704P	PR
PR	22-APR-1998,	98US-082797P	PR
PR	28-APR-1998,	98US-083322P	PR
PR	29-APR-1998,	98US-083493P	PR
PR	29-APR-1998,	98US-083496P	PR
PR	29-APR-1998,	98US-083499P	PR
PR	29-APR-1998,	98US-083559P	PR
PR	05-MAY-1998,	98US-084366P	PR
PR	06-MAY-1998,	98US-084414P	PR
PR	07-MAY-1998,	98US-084639P	PR
PR	07-MAY-1998,	98US-084640P	PR
PR	07-MAY-1998,	98US-084643P	PR
PR	15-MAY-1998,	98US-085579P	PR
PR	15-MAY-1998,	98US-085580P	PR
PR	15-MAY-1998,	98US-085582P	PR
PR	15-MAY-1998,	98US-085700P	PR
PR	28-JUN-1998,	98US-087609P	PR
PR	02-JUN-1998,	98US-087609P	PR
PR	03-JUN-1998,	98US-087759P	PR
PR	03-JUN-1998,	98US-087827P	PR
PR	04-JUN-1998,	98US-088025P	PR
PR	04-JUN-1998,	98US-088028P	PR
PR	04-JUN-1998,	98US-088029P	PR
PR	04-JUN-1998,	98US-088033P	PR
PR	04-JUN-1998,	98US-088036P	PR
PR	05-JUN-1998,	98US-088167P	PR
PR	05-JUN-1998,	98US-088202P	PR
PR	05-JUN-1998,	98US-088212P	PR
PR	05-JUN-1998,	98US-088217P	PR
PR	09-JUN-1998,	98US-088655P	PR

ACA57823
ID ACA57823 standard: cDNA: 1732 bp.

ACA57823;

10-JUN-2003 (first entry)

XX DE Human PRO1557 cDNA. YY

Human; PRO; secreted; transmembrane

KW tumour necrosis factor alpha release
KW differentiation; tumour; gene the
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Homo sapiens.

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PN
US2003036143-A1.

XX PD 20-FEB-2003.

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PF 02-JUL-2002; 2002US-0187600.

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PR 16-SEP-1998; 98WO-US19330.

PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.

PR 08-MAR-1999; 99WO-US05028.
PR 14-MAY-1999; 99WO-US10733.

PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.

PR 15-SEP-1999; 99WO-US21090.
PR 01-DEC-1999; 99WO-US28301.

PR 02-DEC-1999; 99WO-US28551.
PR 30-DEC-1999; 99WO-US31274.

05-JAN-2000; 2000WO-US00219.
18-FEB-2000; 2000WO-US04341.

16. FEB-2000; 2000WO-US043414.
PR
18-FEB-2000; 2000WO-US04342.
PR
22-FEB-2000; 2000WO-US04414.
PR

PR 22-FEB-2000; 2000WO-US05004.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.

PR	01-MAR-2000; 2000WO-US05601.
PR	02-MAR-2000; 2000WO-US05841.

PR 02-MAR-2000; 2000WO-US06841.
PR 15-MAR-2000; 2000WO-US06884.
PR 30-MAR-2000; 2000WO-US08439

EK 30-MAR-2000; 2000WO-US08433.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042

FR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 BB 02-JUN-2000; 2000WO-US15264

PK 02-JUN-2000; 2000WC-US15284.
PR 28-JUL-2000; 2000WC-US20710.
PB 24-AUG-2000; 2000WC-US23328

PR 24-AUG-2000; 2000WC-US23328.
PR 08-NOV-2000; 2000WC-US30952.
PR 01-DEC-2000; 2000WC-US32678.

PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
DE 28 FEB 2001; 2001WO-US06520.

PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 28-FEB-2001; 2001WO-US19692.

PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 20-JUN-2001; 2001WO-US21725.

PR 09-JUL-2001; 2001WO-US21/35.

Query Match		73.9%;	Score 1342.8;	DB 25;	Length 1732;
Best Local Similarity		97.7%;	Pred. No. 0;		
Matches 1362;		Conservative	0;	Mismatches	32; Indels 0; Gaps 0;
Qy	424	TTGGGCTGGAGCTCTCTGGGACTAA	CATGGCACTGGTCGGTTTGGCCAGGCCCCAGACATGT	483	
Db	321	TGGGACTCGCGCTGCTCTGGTTCC	CCCTGGACTCCCAACGCTCGAGCCGCCAGACATGT	380	
Qy	484	TCTGCCTTTTCCATGGGAAGAGATA	CTCCCCGGGAGAGCTGGCACCCTTACTTTGGAGC	543	
Db	381	TCTGCCTTTTCCATGGGAAGAGATA	CTCCCCGGGAGAGCTGGCACCCTTACTTTGGAGC	440	
Qy	544	CACAAGGCGCTGATGTACTGCTGCT	GTACCTGCTCAGAGGGCGCCATGTGATGTTGTT	603	
Db	441	CACAAGGCGCTGATGTACTGCTGCT	GTACCTGCTCAGAGGGCGCCATGTGATGTTGTT	500	
Qy	604	ACCGCTTCCACTGTCCGCTGTCCCA	CTGCCCCAGGCTGTGACGAGGCCACAGCAATGCT	663	
Db	501	ACCGCTTCCACTGTCCGCTGTCCCA	CTGCCCCAGGCTGTGACGAGGCCACAGCAATGCT	560	
Qy	664	GTCCCAAGTGTGGAACTTCACTTCA	CTTCCCTCTGGACTCCGGGGCCCCACCAAGTCTCTGCC	723	
Db	561	GTCCCAAGTGTGGAACTTCACTTCA	CTTCCCTCTGGACTCCGGGGCCCCACCAAGTCTCTGCC	620	
Qy	724	AGCACACGGGACCATGTACCAACAC	CGGAGAGATCTTCACTGCTGCCATGAGCTGTTCCTCT	783	
Db	621	AGCACACGGGACCATGTACCAACAC	CGGAGAGATCTTCACTGCTGCCATGAGCTGTTCCTCT	680	
Qy	784	CCCGCTGCCCAACAGTGTCTCTCT	GCAGCTGCACAGAGGGCCAGATCTACTGCGGCC	843	
Db	681	CCCGCTGCCCAACAGTGTCTCTCT	GCAGCTGCACAGAGGGCCAGATCTACTGCGGCC	740	
Qy	844	TCACAACCTGCCCCGAAACAGGCT	GCCACAGACCCCTCCGCTGCCAGACTCTCTGCTGCC	903	
Db	741	TCACAACCTGCCCCGAAACAGGCT	GCCACAGACCCCTCCGCTGCCAGACTCTCTGCTGCC	800	
Qy	904	AAGCTCTGCAAGATGAGGCAAGTGA	GCATCGATGAAGAGGACAGTGTGCACTGCTCTCC	963	
Db	801	AAGCTCTGCAAGATGAGGCAAGTGA	GCATCGATGAAGAGGACAGTGTGCACTGCTCTCC	860	
Qy	964	ATGGGGTGAGACATCTCAGGATCCT	GTTCAGTGTGCTGGGAGAAAGAGAGGCCCGG	1023	
Db	861	ATGGGGTGAGACATCTCAGGATCCT	GTTCAGTGTGCTGGGAGAAAGAGAGGCCCGG	920	
Qy	1024	GCACCCAGCCCCCACTGGCTCAGGC	CCCCCTTGAGCTTCATCCCTCGCCACTTCAGAC	1083	
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Qy	1084	CCAGGGGAGCAGGACAGCACACTGT	CAAGATCGTCTGAAGGAGAAACATAAGAAAGCT	1143	
Db	981	CCAGGGGAGCAGGACAGCACACTGT	CAAGATCGTCTGAAGGAGAAACATAAGAAAGCT	1040	
Qy	1144	GTGTGCATGGGGGAAAGACGTACT	CCCCAGGGAGGTGTGGCACCCGGCCCTTCGCTGCC	1203	
Db	1041	GTGTGCATGGGGGAAAGACGTACT	CCCCAGGGAGGTGTGGCACCCGGCCCTTCGCTGCC	1100	
Qy	1204	TCGGCCCCCTTGCCCTGATCTCTAT	GCATGTGAGATGGCCCGCCAGGACTGCCAGGCTG	1263	
Db	1101	TCGGCCCCCTTGCCCTGATCTCTAT	GCATGTGAGATGGCCCGCCAGGACTGCCAGGCTG	1160	
Qy	1264	TGACCTGTCCACCGAGTACCCCTGC	CGCTCACCCCGAGAAAGTGGTGGGAGTGTCTGCA	1323	
Db	1161	TGACCTGTCCACCGAGTACCCCTGC	CGCTCACCCCGAGAAAGTGGTGGGAGTGTCTGCA	1220	
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Db	1221	AGATTTGCCAGAGGACAAAGCAGAC	CCCTGGCCACAGTGTGATCAGTTCTTACCAAGGTGT	1280	
Qy	1384	CCAGGGCACCGGGCCGGTCTCTGCT	CCACATCGGTATCCCCAAGCCCCAGACAACTGC	1443	
Db	1281	CCAGGGCACCGGGCCGGTCTCTGCT	CCACATCGGTATCCCCAAGCCCCAGACAACTGC	1340	

RESULT 13
ACA58850
ID ACA58850 standard; cDNA: 1732 BP.

DE cDNA encoding human secret

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OS Homo sapiens.

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PR 14-MAY-1999; 99WO-US10733.

01-MAR-2000; 2000WC-US05801
PR
03-MAR-2000; 2000WC-US05841
PB

PR 02-JUN-2000; 2000WO-US15264.

PR 01-DEC-2000; 2000WO-US32678.
DE 00 DEC 2000 2000WO-US348EC
DE 00 DEC 2000 2000WO-US348EC

PR 01-JUN-2001; ZOOLOGICAL 7500
PR 14-MAY-1999; 99US-0311832.

PR 25-AUG-1999; 99US-0380139.

PR 18-OCT-1999; 99US-0403297;
PR 12-NOV-1999; 99US-0423844;

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The invention relates to an antibody that binds to a polypeptide with a fully defined sequence given in the specification. The methods and compositions (containing antibodies that specifically bind a PRO polypeptide) of the present invention are useful for the preparation of a medicament for the treatment of disorders associated with the aberrant expression or activity of the PRO polypeptide, such as tumour conditions and cancer. They can also be used to generate transgenic or knockout animals useful in the development and screening of therapeutically useful reagents. The PRO polypeptides and encoding nucleic acids can be used as molecular weight markers for protein electrophoresis, chromosome identification and tissue typing. The PRO polypeptides are useful to induce angiogenesis *e.g* wound healing; in the treatment of sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis; diabetes, hyperinsulinaemia and hypoinsulinaemia. The antibodies may be used in various diagnostic, competitive binding and/or immunoprecipitation assays. The present sequence represents a cDNA encoding a PRO polypeptide of the invention.

Sequence 1732 BP: 369 A: 592 C: 425 G: 346 T: 0 other:

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      73.9%; Score 1342.8; DB 25; Length 1732;
      Local Similarity 97.7%; Pred. No. 0;
      Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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424 TTCTGGCTGGAGCCCTCTGGGACTAACATGGCACTGGTCGGTTTCCAGGCCAGACATGT 483

380 CACGACATGT

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[illegible]

381 TCTGCCCTTTTCCATGGGAAGAGATACTCCCCGGCGAGAGCTGGACCCCTACCTGGAGC 440

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724 AGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAAGTGCCTCATAGCTGTTCCTCT 783
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621 AGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAAGTGCCTCATAGCTGTTCCTCT 680
784 CCCGCTTGGCCCAACACAGTGTGTCTCTGACGTGCACAGAGGCGCAGATCTACTGCGGCC 843
785 |||||
681 CCCGCTTGGCCCAACACAGTGTGTCTCTGACGTGCACAGAGGCGCAGATCTACTGCGGCC 740
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1504 TAAAGATGAGAACTGAGGCTCAGAGGTGAAGTACTCTGCCCCAAGGCCACAGCC 1563
1401 TAAAGATGAGAACTGAGGCTCAGAGGTGAAGTACTCTGCCCCAAGGCCACAGCC 1460
1564 AGATCTTCCACTTGACTCAGATCAGAAAGTTCAGGAACAGACTTCCAGAAAGGCA 1623
1461 AGATCTTCCACTTGACTCAGATCAGAAAGTTCAGGAACAGACTTCCAGAAAGGCA 1520
1624 CAGCACTTCCGACTGCTCGCTGGCCCCCAGCAAGGTCACTGGAACCTCTCTAGGCCAG 1683
1521 CAGCACTTCCGACTGCTCGCTGGCCCCCAGCAAGGTCACTGGAACCTCTCTAGGCCAG 1580
1684 ACCCTGGAGCTGAAGGTCAAGGCTCAGGCTCAGCAAAAGTGAAGCAAGACATAAAGAACCT 1743
1581 ACCCTGGAGCTGAAGGTCAAGGCTCAGGCTCAGCAAAAGTGAAGCAAGACATAAAGAACCT 1640
1744 AACAGTTCAGATGAGCTGATTAATTTGTTGTTATTAATTAATAAATAAGAGTTG 1803
1641 AACAGTTCAGATGAGCTGATTAATTTGTTGTTATTAATTAATAAATAAGAGTTG 1700
1804 CATAACCATCAAAA 1817

Db 1701 CATTACCCTCAAA 1714
RESULT 14
ACA60403
ID ACA60403 standard; cDNA; 1732 BP.
XX
AC ACA60403;
XX
DT 11-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1557 cDNA.
XX
KW Human; secreted and transmembrane polypeptide; gene; ss.
KW chromosome mapping; gene mapping; transgenic animal; knockout animal;
KW therapeutic agent screening; chromosome identification; tissue typing;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN US2003018183-A1.
XX
PD 23-JAN-2003.
XX
PF 01-MAY-2002; 2002US-0063512.
XX
PR 06-DEC-2001; 2001US-0006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-330984/31.
DR P-PSDB; ABU71992.
XX
XX New secreted and transmembrane PRO polypeptides and nucleic acid
PT molecules encoding the polypeptides, useful in gene therapy or
PT preparing a medicament for treating a condition that is responsive to
PT the PRO polypeptide or antibody -
XX
PS Disclosure; Fig 81; 409pp; English.
XX
CC The invention describes novel isolated PRO polypeptides. The PRO
CC polypeptides or anti-PRO antibodies are useful in preparing a medicament
CC for treating a condition that is responsive to the PRO polypeptide or
CC antibody. The PRO nucleotide sequences may be used as hybridisation
CC probes in chromosome and gene mapping, or in generating antisense RNA
CC and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides,
CC in assays to identify other proteins or molecules involved in binding
CC reaction, to generate transgenic animals or knockout animals, which in
CC turn are useful in the development and screening of therapeutically
CC useful reagents, for chromosome identification, and tissue typing. The
CC PRO polypeptides and nucleic acid molecules are also useful in gene
CC therapy, and as molecular weight markers for protein electrophoresis
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
CC PRO, or for the affinity purification of PRO from recombinant cell
CC culture or natural sources. This sequence encodes a novel human
CC secreted and transmembrane PRO polypeptide.
XX
SQ Sequence 1732 BP; 369 A; 592 C; 425 G; 346 T; 0 other;

Query Match 73.9%; Score 1342.8; DB 25; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 424 TTGGCTGGACCTCTCGGACTACATGGCACTGGTTCGGTTTCCAGGCCCGACACATGT 483
Db 321 TGGACTCGCTGCTCTGGTTCCCTTCCGATCCACCGCTCGAGCCCGCCAGACATGT 380
QY 484 TCTGCTTTCCATGGGAAGATGATCTCCCGCGGAGAGCTGGACCCCTACTTGGAGC 543

381	TCTGCCCTTTTCC	AGAGAT	CTCC	CCGGCAGAG	CTGGCA	CCCCCTACTTTGGAGC	440
544	CACAAGGCCTGAT	TACTGCCT	CGCGTGTAC	CTTGCTCAGAGGG	CGCCATCTGAGTTCGTT	603	
441	CACAAGGCCTGAT	GTACTGCT	CGCGTGTAC	CTTGCTCAGAGGG	CGCCATCTGAGTTCGTT	500	
604	ACCGCCTCCACT	GTCCGCTGT	CTCACTGCC	CCAGCCTGTGACGGAG	CCACAGCAATGCT	663	
501	ACCGCCTCCACT	GTCCGCTGT	CTCACTGCC	CCAGCCTGTGACGGAG	CCACAGCAATGCT	560	
664	GTCCCAAGTGT	GTGAACCT	CTCACTCCCT	CTGGA	CTCCGGGCCCCACCAAGTCTCTGCC	723	
561	GTCCCAAGTGT	GTGAACCT	CTCACTCCCT	CTGGA	CTCCGGGCCCCACCAAGTCTCTGCC	620	
724	AGCAAAACGGG	ACCATGTACCA	ACAGGAGAT	CTTCAGTGGCC	ATGAGCTGTTCCCT	783	
621	AGCAAAACGGG	ACCATGTACCA	ACAGGAGAT	CTTCAGTGGCC	ATGAGCTGTTCCCT	680	
784	CCCGCTGCC	CAACAGTGT	CTCTG	CAGCTGCA	CAGAGGGCCAGATCTACTTCGGGCC	843	
681	CCCGCTGCC	CAACAGTGT	CTCTG	CAGCTGCA	CAGAGGGCCAGATCTACTTCGGGCC	740	
844	TCACAACCTG	CCCCGAACAGG	CTGCCAGCA	CCCCCTCCCGCTG	CCAGACTCTCTGCTGCC	903	
741	TCACAACCTG	CCCCGAACAGG	CTGCCAGCA	CCCCCTCCCGCTG	CCAGACTCTCTGCTGCC	800	
904	AAGCCTGCA	AAGATGAGGCA	AGTGA	CGAATCGATGA	AGAGCAAGTGTGCAGTGCCTGCC	963	
801	AAGCCTGCA	AAGATGAGGCA	AGTGA	CGAATCGATGA	AGAGCAAGTGTGCAGTGCCTGCC	860	
964	ATGGGTTGAGA	CATCTCAGGAT	CCATGTTCC	AGTGTGCTGGAGAA	AGAGAGGCCCGG	1023	
861	ATGGGTTGAGA	CATCTCAGGAT	CCATGTTCC	AGTGTGCTGGAGAA	AGAGAGGCCCGG	920	
1024	GCACCCAGC	CCCCCACTGG	CTGGCTCAG	CGCCCCCTCTGAGCTT	CATCCCTCGCCACTTTCAGAC	1083	
921	GCACCCAGC	CCCCCACTGG	CTGGCTCAG	CGCCCCCTCTGAGCTT	CATCCCTCGCCACTTTCAGAC	980	
1084	CCAAGGGAC	GCAGCACA	AACTGTCA	AGATCGTCTGAAGAGAA	CATAGAAGAGCCT	1143	
981	CCAAGGGAC	GCAGCACA	AACTGTCA	AGATCGTCTGAAGAGAA	CATAGAAGAGCCT	1040	
1144	GTGTGATGG	CGGGAAGAG	CTACTCCCA	CGGGGAGGTGTGGCA	CCCCGCCCTTCCGTGCC	1203	
1041	GTGTGATGG	CGGGAAGAG	CTACTCCCA	CGGGGAGGTGTGGCA	CCCCGCCCTTCCGTGCC	1100	
1204	TGGGCCCTT	GCCCTGCAT	CCTATGCA	CTGTAGGATGG	CGCCAGGACTGCCAGCTG	1263	
1101	TGGGCCCTT	GCCCTGCAT	CCTATGCA	CTGTAGGATGG	CGCCAGGACTGCCAGCTG	1160	
1264	TGACCTGT	CCCAACGAG	TACCCCTG	CGGTACCCCGGAGAA	AGTGTGCTGGAAAGTGTGCA	1323	
1161	TGACCTGT	CCCAACGAG	TACCCCTG	CGGTACCCCGGAGAA	AGTGTGCTGGAAAGTGTGCA	1220	
1324	AGATTGCC	CAGAGGA	CAAAAGCAG	ACCTTGGCCCA	CAGTGCAGTTCAGTTCACAGGTC	1383	
1221	AGATTGCC	CAGAGGA	CAAAAGCAG	ACCTTGGCCCA	CAGTGCAGTTCAGTTCACAGGTC	1280	
1384	CCAAGGCA	CCGGGCGGGT	CTCGTCC	ACACATCGGTAT	CCCCAAGCCACAGCAACCTGC	1443	
1281	CCAAGGCA	CCGGGCGGGT	CTCGTCC	ACACATCGGTAT	CCCCAAGCCACAGCAACCTGC	1340	
1444	GTGCTTTG	CCCTGGAA	CAAGAGG	CCCTCGGACTTGGT	GGAGATCTACCTCTGGAAAGCTGG	1503	
1341	GTGCTTTG	CCCTGGAA	CAAGAGG	CCCTCGGACTTGGT	GGAGATCTACCTCTGGAAAGCTGG	1400	
1504	TAAAGATG	AGGAAACT	GAGGCTCAG	AGAGGTGA	AGTACTTGGCCCCAAGGCCACAGCC	1563	
1401	TAAAGATG	AGGAAACT	GAGGCTCAG	AGAGGTGA	AGTACTTGGCCCCAAGGCCACAGCC	1460	
1564	AGAACTT	TCCACTTGA	CTCAGATCA	AGAAAGT	TCAGGAAGCAAGACTTCCAGAAAGAGGCA	1623	
1461	AGAACTT	TCCACTTGA	CTCAGATCA	AGAAAGT	TCAGGAAGCAAGACTTCCAGAAAGAGGCA	1520	

Qy	1624	CAGCACTTCGCACTGCTCGTGGCCGCCCCACGAAAGGTCACTGGAAGCTCTTCCTAGCCCCAG	1680
Db	1521	CAGCACTTCGCACTGCTCGTGGCCGCCCCACGAAAGGTCACTGGAAGCTCTTCCTAGCCCCAG	1580
Qy	1684	ACCCTGGAGCTCAAGGTCACGGCCAGTCCAGACAAAGTGACCAAGACATATAACAAAGACCT	1743
Db	1581	ACCCTGGAGCTCAAGGTCACGGCCAGTCCAGACAAAGTGACCAAGACATATAACAAAGACCT	1640
Qy	1744	AACAGTTGCAGATATGAGCTGTATATAATTTGTTTATTATATATATTAATTAATAAGAAGTTG	1803
Db	1641	AACAGTTGCAGATATGAGCTGTATATAATTTGTTTATTATATATATTAATTAATAAGAAGTTG	1700
Qy	1804	CATAACCATCAAAA	1817
Db	1701	CAATACCCCTCAAAA	1714
RESULT 15			
ACAG63413			
ID	ACAG63413 standard; cDNA; 1732 BP.		
XX	ACAG63413;		
XX	13-JUN-2003 (first entry)		
XX	cDNA encoding human PRO polypeptide #41.		
DE	Human; PRO polypeptide; secreted and transmembrane protein;		
XX	anti-PRO antibody; diagnostic assay; gene expression; gene; ss.		
KW	Homo sapiens.		
OS	US2003023042-A1.		
XX	30-JAN-2003.		
PN	01-MAY-2002; 2002US-0063502.		
XX	06-DEC-2001; 2001US-0006867.		
PF	(GETH) GENENTECH INC.		
XX	Eaton DL, Filvaroff E, Gerzitsen ME, Goddard A, Godowski PJ;		
PA	Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;		
PI	WPI; 2003-331484/31.		
PI	P-PSDB; ABU72149.		
XX	Novel monoclonal antibody that binds to secreted and transmembrane		
PT	polypeptide, useful for detecting and purifying the polypeptide and		
PT	also for treating conditions responsive to the antibody -		
XX	Disclosure; Fig 81; 408pp; English.		
PS	The present invention relates to the isolation of novel human PRO		
XX	polypeptides, and the polynucleotide sequences encoding them. The		
CC	PRO polypeptides are secreted and transmembrane proteins. The PRO		
CC	polypeptides and polynucleotides are useful for preparing a		
CC	medicament useful in the treatment of a condition responsive to		
CC	anti-PRO antibody. Anti-PRO antibodies are useful in diagnostic		
CC	assays for PRO, by detecting its expression in specific cells,		
CC	tissues or serum, and for affinity purification of PRO from		
CC	recombinant cell culture or natural sources. ACA63373-ACA63456		
CC	represent cDNA sequences encoding the human PRO polypeptides of		
CC	the invention.		
XX	Sequence 1732 BP; 369 A; 592 C; 425 G; 346 T; 0 other;		
SO			

Query Match	73.9%;	Score 1342.8;	DB 25;	Length 1732;
Best Local Similarity	97.7%;	Pred. NO. 0;		
Matches 1362;	Conservative	0;	Mismatches	32;
			Indels	0;
			Gaps	0;

PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 18-SEP-1997; 97US-059263P.
PR 18-SEP-1997; 97US-059266P.
PR 17-OCT-1997; 97US-062250P.
PR 21-OCT-1997; 97US-063486P.
PR 24-OCT-1997; 97US-063120P.
PR 24-OCT-1997; 97US-063121P.
PR 28-OCT-1997; 97US-063540P.
PR 28-OCT-1997; 97US-063541P.
PR 28-OCT-1997; 97US-063544P.
PR 28-OCT-1997; 97US-063564P.
PR 29-OCT-1997; 97US-063734P.
PR 31-OCT-1997; 97US-063870P.
PR 31-OCT-1997; 97US-064103P.
PR 13-NOV-1997; 97US-065311P.
PR 21-NOV-1997; 97US-066120P.
PR 24-NOV-1997; 97US-066466P.
PR 24-NOV-1997; 97US-066772P.
PR 11-DEC-1997; 97US-069335P.
PR 12-DEC-1997; 97US-069425P.
PR 17-DEC-1997; 97US-069870P.
PR 18-DEC-1997; 97US-068017P.
PR 10-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077632P.
PR 11-MAR-1998; 98US-077649P.
PR 20-MAR-1998; 98US-078886P.
PR 27-MAR-1998; 98US-079664P.
PR 27-MAR-1998; 98US-079786P.
PR 31-MAR-1998; 98US-080107P.
PR 31-MAR-1998; 98US-080194P.
PR 01-APR-1998; 98US-080327P.
PR 01-APR-1998; 98US-080333P.
PR 08-APR-1998; 98US-081049P.
PR 08-APR-1998; 98US-081070P.
PR 09-APR-1998; 98US-081195P.
PR 15-APR-1998; 98US-081838P.
PR 21-APR-1998; 98US-082568P.
PR 21-APR-1998; 98US-082569P.
PR 22-APR-1998; 98US-082704P.
PR 22-APR-1998; 98US-082797P.
PR 28-APR-1998; 98US-083322P.
PR 29-APR-1998; 98US-083495P.
PR 29-APR-1998; 98US-083496P.
PR 29-APR-1998; 98US-083499P.
PR 29-APR-1998; 98US-083559P.
PR 05-MAY-1998; 98US-084366P.
PR 06-MAY-1998; 98US-084414P.
PR 07-MAY-1998; 98US-084639P.
PR 07-MAY-1998; 98US-084640P.
PR 07-MAY-1998; 98US-084643P.
PR 15-MAY-1998; 98US-085579P.
PR 15-MAY-1998; 98US-085580P.
PR 15-MAY-1998; 98US-085582P.
PR 15-MAY-1998; 98US-085700P.
PR 18-MAY-1998; 98US-086023P.
PR 22-MAY-1998; 98US-086392P.
PR 22-MAY-1998; 98US-086486P.
PR 28-MAY-1998; 98US-087098P.
PR 28-MAY-1998; 98US-087208P.
PR 02-JUN-1998; 98US-087609P.
PR 02-JUN-1998; 98US-087759P.
PR 03-JUN-1998; 98US-087827P.
PR 04-JUN-1998; 98US-088025P.
PR 04-JUN-1998; 98US-088028P.
PR 04-JUN-1998; 98US-088029P.
PR 04-JUN-1998; 98US-088033P.
PR 05-JUN-1998; 98US-088326P.
PR 05-JUN-1998; 98US-088167P.
PR 05-JUN-1998; 98US-088202P.
PR 05-JUN-1998; 98US-088212P.
PR 05-JUN-1998; 98US-088217P.
PR 09-JUN-1998; 98US-088655P.
PR 10-JUN-1998; 98US-088722P.
PR 10-JUN-1998; 98US-088738P.
PR 10-JUN-1998; 98US-088740P.
PR 10-JUN-1998; 98US-088811P.
PR 10-JUN-1998; 98US-088824P.
PR 10-JUN-1998; 98US-088825P.
PR 10-JUN-1998; 98US-088826P.
PR 11-JUN-1998; 98US-088861P.
PR 11-JUN-1998; 98US-088863P.
PR 11-JUN-1998; 98US-088876P.
PR 12-JUN-1998; 98US-089090P.
PR 12-JUN-1998; 98US-089105P.
PR 16-JUN-1998; 98US-089512P.
PR 16-JUN-1998; 98US-089514P.
PR 17-JUN-1998; 98US-089538P.
PR 17-JUN-1998; 98US-089598P.
PR 17-JUN-1998; 98US-089653P.
PR 18-JUN-1998; 98US-089908P.
PR 19-JUN-1998; 98US-089952P.
PR 22-JUN-1998; 98US-090246P.
PR 22-JUN-1998; 98US-090252P.
PR 22-JUN-1998; 98US-090254P.
PR 24-JUN-1998; 98US-090429P.
PR 24-JUN-1998; 98US-090435P.
PR 24-JUN-1998; 98US-090444P.
PR 24-JUN-1998; 98US-090461P.
PR 24-JUN-1998; 98US-090535P.
PR 24-JUN-1998; 98US-090540P.
PR 25-JUN-1998; 98US-090676P.
PR 25-JUN-1998; 98US-090678P.
PR 25-JUN-1998; 98US-090688P.
PR 25-JUN-1998; 98US-090690P.
PR 25-JUN-1998; 98US-090694P.
PR 25-JUN-1998; 98US-090695P.
PR 25-JUN-1998; 98US-090696P.
PR 26-JUN-1998; 98US-090862P.
PR 26-JUN-1998; 98US-090863P.
PR 26-JUN-1998; 98US-091010P.
PR 01-JUL-1998; 98US-091359P.
PR 01-JUL-1998; 98US-091544P.
PR 02-JUL-1998; 98US-091478P.
PR 02-JUL-1998; 98US-091486P.
PR 02-JUL-1998; 98US-091628P.
PR 02-JUL-1998; 98US-091628P.
PR 02-JUL-1998; 98US-091632P.
PR 24-JUL-1998; 98US-094006P.
PR 04-AUG-1998; 98US-095282P.
PR 10-AUG-1998; 98US-095998P.
PR 10-AUG-1998; 98US-096012P.
PR 17-AUG-1998; 98US-096757P.
PR 17-AUG-1998; 98US-096766P.
PR 17-AUG-1998; 98US-096867P.
PR 17-AUG-1998; 98US-096891P.
PR 17-AUG-1998; 98US-096897P.
PR 18-AUG-1998; 98US-096949P.
PR 18-AUG-1998; 98US-096959P.
PR 18-AUG-1998; 98US-097022P.
PR 26-AUG-1998; 98US-097952P.
PR 26-AUG-1998; 98US-097954P.
PR 26-AUG-1998; 98US-097955P.
PR 26-AUG-1998; 98US-097971P.
PR 26-AUG-1998; 98US-097974P.
PR 26-AUG-1998; 98US-098014P.

Query Match		73.9%	Score 1342.8	DB 25	Length 1732
Best Local Similarity		97.7%	Pred. No. 0		
Matches 1362		Conservative 0	Mismatches 32	Indels 0	Gaps 0
Y	424	TTGGGCTGGAGCCCTCTGGGACTAACATGGCACTGGTTCGGTTTGGCCAGCCCGACATGT	483		
b	321	TGGGACTCGCGCTGCTGCTGCTTCCCTTGACTCCACGCTCGAGCCCGCCACAGATGT	380		
Y	484	TTGCTCTTTTCCATGGGAAGAGATACTCCCGGGGAGAGCTGGCACCCCTACTTTGGAGC	543		
b	381	TCTGCTTTTCCATGGGAAGAGATACTCCCGGGGAGAGCTGGCACCCCTACTTTGGAGC	440		
Y	544	CACAAGGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	603		
b	441	CACAAGGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	500		
Y	604	ACGCGCTCCACTGTCGCGCTCTCCACTGCGCCCTGCGCCCTGCGCCCTGCGCCCTGCGCC	663		
b	501	ACGCGCTCCACTGTCGCGCTCTCCACTGCGCCCTGCGCCCTGCGCCCTGCGCCCTGCGCC	560		
Y	664	GTCCCAAGTGTGCGAACTCACACTCCCTCTGGACTCCGCGCCCGCCACCAAGTCTCTGCC	723		
b	561	GTCCCAAGTGTGCGAACTCACACTCCCTCTGGACTCCGCGCCCGCCACCAAGTCTCTGCC	620		
Y	724	AGCACAAACGGGACCATGTATACCAACACGAGAGATCTTCAGTCCCATGAGCTGTTCCTT	783		
b	621	AGCACAAACGGGACCATGTATACCAACACGAGAGATCTTCAGTCCCATGAGCTGTTCCTT	680		
Y	784	CCGCGCTGCGCAACAGTGTCTCTGAGCTGTCGAGGTGCACAGAGGCGGCGAGTCTACTGGG	843		
b	681	CCGCGCTGCGCAACAGTGTCTCTGAGCTGTCGAGGTGCACAGAGGCGGCGAGTCTACTGGG	740		
Y	844	TCACAACTGCGCGCAACAGTGTCTCTGAGCTGTCGAGGTGCACAGAGGCGGCGAGTCTCTG	903		
b	741	TCACAACTGCGCGCAACAGTGTCTCTGAGCTGTCGAGGTGCACAGAGGCGGCGAGTCTCTG	800		
Y	904	AAGCTTCAAGATGAGGCAAGTGTGAGCAATCGATGAAGAGACAGTGTGAGTGTCTCTCC	963		
b	801	AAGCTTCAAGATGAGGCAAGTGTGAGCAATCGATGAAGAGACAGTGTGAGTGTCTCTCC	860		
Y	964	ATGGGTGTGACATCTCTCAGGATCCATGTTCCAGTGTGCTGGGAGAAAGAGAGGCGCGG	1023		
b	861	ATGGGTGTGACATCTCTCAGGATCCATGTTCCAGTGTGCTGGGAGAAAGAGAGGCGCGG	920		
Y	1024	GCACCCAGCCCGCACTGGCTCTAGCGCCCTCTGAGCTTCACTCTGCGCACTTCAGAC	1083		
b	921	GCACCCAGCCCGCACTGGCTCTAGCGCCCTCTGAGCTTCACTCTGCGCACTTCAGAC	980		
Y	1084	CCAAGGAGCAGGACGACACTGTCAAGATGCTCTGAGGAGAGAACTAAGAAGCTT	1143		
b	981	CCAAGGAGCAGGACGACACTGTCAAGATGCTCTGAGGAGAGAACTAAGAAGCTT	1040		
Y	1144	GTGTGATGCGGGAAGACGCTACTCCACGCGGAGGTGTGGACCCGCTTCCGTCCT	1203		
b	1041	GTGTGATGCGGGAAGACGCTACTCCACGCGGAGGTGTGGACCCGCTTCCGTCCT	1100		
Y	1204	TCGGCCCTTTCCTTGCATCTATGACCTGTGAGGATGGCCCGCAGGACTGCCAGCTG	1263		
b	1101	TCGGCCCTTTCCTTGCATCTATGACCTGTGAGGATGGCCCGCAGGACTGCCAGCTG	1160		
Y	1264	TGACCTGTCCACGAGTACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1323		
b	1161	TGACCTGTCCACGAGTACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1220		
Y	1324	AGATTGCCCCAGAGACAAAGCAGACCCCTGGCCACAGTGTGAGTCTTACCAGGTGTC	1383		

Db	1221	AGATTGCCCCAGAGGACAAAGCAGACCCCTGGCCACAGTGTGATCAGTTCTACCAAGTGTG	1280
Qy	1384	CAAAGGCAACCGGCGCGGTCTCTGCTCCACATCGGTATCCCAAGCCCGACAACTGTC	1443
Db	1281	CAAAGGCAACCGGCGCGGTCTCTGCTCCACATCGGTATCCCAAGCCCGACAACTGTC	1340
Qy	1444	GTCCCTTTGCTGCTGAAACACGAGGCGCTCGGACTTGGTGGAGTCTACCTTGGAGCTGG	1503
Db	1341	GTCCCTTTGCTGCTGAAACACGAGGCGCTCGGACTTGGTGGAGTCTACCTTGGAGCTGG	1400
Qy	1504	TAAAGATGAGGAAACTGAGGCTCAGAGAGGTGAAGTCTCTGCGCCCAAGCCACACAGCC	1563
Db	1401	TAAAGATGAGGAAACTGAGGCTCAGAGAGGTGAAGTCTCTGCGCCCAAGCCACACAGCC	1460
Qy	1564	AGAACTTCTTCACTGACTCAGATCAAGAAAGTCAGGAAGCAAGCTTCCAGAAAGAGCA	1623
Db	1461	AGAACTTCTTCACTGACTCAGATCAAGAAAGTCAGGAAGCAAGCTTCCAGAAAGAGCA	1520
Qy	1624	CAGCACTTCCAGCTGCTGCTGCGCCCGCCACGAAAGTCACTGGAACGTCTTCTAGCCGAG	1683
Db	1521	CAGCACTTCCAGCTGCTGCTGCGCCCGCCACGAAAGTCACTGGAACGTCTTCTAGCCGAG	1580
Qy	1684	ACCTTGGAGCTGAAGTCAAGGCTCAGGCTCAGCAAGAGTCCAGCAAGATCAACAAAGACCT	1743
Db	1581	ACCTTGGAGCTGAAGTCAAGGCTCAGGCTCAGCAAGAGTCCAGCAAGATCAACAAAGACCT	1640
Qy	1744	AACAGTTCGAGATATGAGCTGTATTAATTTGTTTATTATATATATATATATATATATAT	1803
Db	1641	AACAGTTCGAGATATGAGCTGTATTAATTTGTTTATTATATATATATATATATATATAT	1700
Qy	1804	CATAACCATCAAAA 1817	
Db	1701	CATTACCCTCAAAA 1714	
RESULT 17			
ABX98795	ID	ABX98795 standard; cDNA; 1732 BP.	
XX	AC	ABX98795;	
XX	DT	20-MAY-2003 (first entry)	
XX	DE	Novel human secreted and transmembrane protein PRO1557 cDNA.	
XX	KW	Human; secreted protein; transmembrane protein; cytostatic;	
XX	KW	gene therapy; TNF-Agonist-Alpha; chondrocyte stimulator; tumour;	
XX	KW	adrenal tumour; lung tumour; colon tumour; breast tumour;	
XX	KW	prostate tumour; rectal tumour; cervical tumour; liver tumour;	
XX	OS	Gene; ss.	
XX	OS	Homo sapiens.	
XX	PN	US2003036157-A1.	
XX	PD	20-FEB-2003.	
XX	PF	02-JUL-2002; 2002US-0188769.	
XX	PR	16-SEP-1998; 98WO-US19330.	
XX	PR	07-OCT-1998; 98WO-US21141.	
XX	PR	01-DEC-1998; 98WO-US25108.	
XX	PR	08-MAR-1999; 99WO-US05028.	
XX	PR	14-MAY-1999; 99WO-US10733.	
XX	PR	02-JUN-1999; 99WO-US12252.	
XX	PR	01-SEP-1999; 99WO-US20111.	
XX	PR	15-SEP-1999; 99WO-US21090.	
XX	PR	01-DEC-1999; 99WO-US28301.	
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y	1084	CCAAGGGAGCAGCAGCAACAATGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCT	1143
b	981	CCAAGGGAGCAGCAGCAACAATGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCT	1040
y	1144	GTGTGCATGGCGGGAGAGCTACTCCACGGGAGGTGTGGCACCGCGGCTTCCGTGCGCT	1203
b	1041	GTGTGCATGGCGGGAGAGCTACTCCACGGGAGGTGTGGCACCGCGGCTTCCGTGCGCT	1100
y	1204	TGGGCCCTTGGCCCTGCATCTTATGACCTGTGAGATGGCGGCCAGAGCTGCGACGCGTG	1263
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y	1264	TGACCTGTCCACCGAGTACCCCTGCGGTCACCCAGAGAAAGTGGGTGGGAAGTGTGCA	1323
b	1161	TGACCTGTCCACCGAGTACCCCTGCGGTCACCCAGAGAAAGTGGGTGGGAAGTGTGCA	1220
y	1324	AGATTGTGCCACGAGACAAGCAGACCCCTGGCCACAGTCAGATCAGTTCACAGGTGC	1383
b	1221	AGATTGTGCCACGAGACAAGCAGACCCCTGGCCACAGTCAGATCAGTTCACAGGTGC	1280
y	1384	CCAAGGCACCGGCGGGTCTCGTCCACACATCGGTATCCCCCAAGCCACAGCAACCTGC	1443
b	1281	CCAAGGCACCGGCGGGTCTCGTCCACACATCGGTATCCCCCAAGCCACAGCAACCTGC	1340
y	1444	GTGCGTTTGCCTTGGAAACACGAGGCTCGGACTTGGTGAGATCTACCTCTGGAAGCTG	1503
b	1341	GTGCGTTTGCCTTGGAAACACGAGGCTCGGACTTGGTGAGATCTACCTCTGGAAGCTG	1400
y	1504	TAAAGATGAGGAAACTGAGGCTCAGAGAGGTGAAGTACTCGGCCCAAGGCCACAGCC	1563
b	1401	TAAAGATGAGGAAACTGAGGCTCAGAGAGGTGAAGTACTCGGCCCAAGGCCACAGCC	1460
y	1564	AGAATCTTCCACTTGACTCAGATCAGAAAGTCAGGAAGCAAGACTTCCAGAAAGGCA	1623
b	1461	AGAATCTTCCACTTGACTCAGATCAGAAAGTCAGGAAGCAAGACTTCCAGAAAGGCA	1520
y	1624	CAGCACTTCCGACTGCTCGCTGCGCCCCCAGGAAGTCACTGGAAAGCTTCTTAGCCCCAG	1683
b	1521	CAGCACTTCCGACTGCTCGCTGCGCCCCCAGGAAGTCACTGGAAAGCTTCTTAGCCCCAG	1580
y	1684	ACCTTGGAGCTGAAGGTCAAGGTCAAGGTCCAGCAAAAGTCAGCAAGACATAACAAGACCT	1743
b	1581	ACCTTGGAGCTGAAGGTCAAGGTCAAGGTCCAGCAAAAGTCAGCAAGACATAACAAGACCT	1640
y	1744	AACAGTTCAGATATGAGCTGTATAATTGTTGTTATTTATTTATTTATTAATAAAGAGTTG	1803
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W	protein electrophoresis; tumour necrosis factor-alpha; TNP-alpha; blood;		
W	chondrocyte differentiation; chondrocyte proliferation; tumour.		
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b 801 AAGCCTGCAAGATGAGCGAAGTGAAGCAATCGATGAAGAGACAGTGTGCACTGCCTCC 860
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b 861 ATGGGGTGACATCCTCAGATCCATGTTCCAGTGTCTGGGAGAAAGAGAGAGCCCGG 920
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b 921 GCACCCCGACCCCTCCACTGCGCTCAGCGCCCTCTGAGCTTCATCCTCGCCACTTTCAGAC 980
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b 981 CCAAGGAGCAGGACGACACAACTGTCAAGATCGTCTGAAGAGAGAAACATAGAAGCCT 1040
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b 1281 CCAAGCAGCGGCGCGGTCTCTGCTGCACATCGGTATCCCAAGCCAGACACCTTGC 1340
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Y 1684 ACCCTGGAGTGAAGTCAAGGCTCAGAGAGGTGCAAGAAAGTCAAGACATACAAAGCCT 1743
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BX78668

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X C ABX78668;

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DT 15-APR-2003 (first entry)
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DE Human; PRO; gene; ss; cytostatic; tumour; cancer; breast; lung; stomach;
KW liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodruug therapy.
XX OS Homo sapiens.
XX US2003027272-A1.
XX PN 06-FEB-2003.
XX PD 21-JUN-2002; 2002US-0176492.
XX PF 15-SEP-1998; 98WO-US19330.
XX PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
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PR 21-OCT-1997; 97US-063486P.
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Db 1701 CATTACCTCAAAA 1714
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XX chondrocyte cell proliferation; chondrocyte cell differentiation;
XX tumour; adrenal tumour; lung tumour; colon tumour; breast tumour;
XX prostate tumour; rectal tumour; cervical tumour; liver tumour;
XX bone disorder; cartilage disorder; arthritis; sports injury.
OS Homo sapiens.
XX US2003022298-A1.
PN 30-JAN-2003.
XX 20-JUN-2002; 2002US-0176913.
XX 05-NOV-1997; 97WO-US20069.
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921	D	GCACCCAGCCCCACATGGCTCTCAG	CGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC	980
1084	Y	CCAAGGGAGCAGGCAGCAACAATGT	CAAGATCGTCTGAAGAGAGAAACATAAGAAAGCCT	1143
981	D	CCAAGGGAGCAGGCAGCAACAATGT	CAAGATCGTCTGAAGAGAGAAACATAAGAAAGCCT	1040
1144	Y	GTGTGCATGGCGGAAGACGTACTCC	CAACGGGAGGTGTGGCAACCGGCCCTTCCTGTCCT	1203
1041	D	GTGTGCATGGCGGAAGACGTACTCC	CAACGGGAGGTGTGGCAACCGGCCCTTCCTGTCCT	1100
1204	Y	TCGGCCCCCTTGCCTGCATCTATG	CACTGTGAGATGGCGCCGACAGACTGCCAGGTG	1263
1101	D	TCGGCCCCCTTGCCTGCATCTATG	CACTGTGAGATGGCGCCGACAGACTGCCAGGTG	1160
1264	Y	TGACCTGTCCACACGAGTACCCCTG	CTCCAGCAACAGTGGCTGGGAAAGTGTGCTGCA	1323
1161	D	TGACCTGTCCACACGAGTACCCCTG	CTCCAGCAACAGTGGCTGGGAAAGTGTGCTGCA	1220
1324	Y	AGATTTCGCCAGAGCAAAAGCAGAC	CCCTGGCCACAGTGAGATCAGTTCTTACCAAGTGTG	1383
1221	D	AGATTTCGCCAGAGCAAAAGCAGAC	CCCTGGCCACAGTGAGATCAGTTCTTACCAAGTGTG	1280
1384	Y	CCAAAGCACCGGGCCGGTCTCTGTG	TCACACATCGGTATCCCCAAAGCCACAGCAACCTGC	1443
1281	D	CCAAAGCACCGGGCCGGTCTCTGTG	TCACACATCGGTATCCCCAAAGCCACAGCAACCTGC	1340

Qy	1444	GTGCGTTTGGCCCTGGAAACACGAGGCGCTCGGACCTTGGTGGAGATCTACCTCTCGAAAGCTGG	1503
Db	1341	GTGCGTTTGGCCCTGGAAACACGAGGCGCTCGGACCTTGGTGGAGATCTACCTCTCGAAAGCTGG	1400
Qy	1504	TAAAGATGAGGAAACTGAGGGCTCAGAGAGGTGAAGTACCTTGGCCCAAGGCCACACAGCC	1563
Db	1401	TAAAGATGAGGAAACTGAGGGCTCAGAGAGGTGAAGTACCTTGGCCCAAGGCCACACAGCC	1460
Qy	1564	AGAACTCTTCCACTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCCA	1623
Db	1461	AGAACTCTTCCACTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCCA	1520
Qy	1624	CAGCACTTCCGACTGCTCGCTGCGCCGCCCCACGAAAGTCACTGGAACGTCTTCTTAGCCCGAG	1683
Db	1521	CAGCACTTCCGACTGCTCGCTGCGCCGCCCCACGAAAGTCACTGGAACGTCTTCTTAGCCCGAG	1580
Qy	1684	ACCCCTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAGACATATAACAAAGACCT	1743
Db	1581	ACCCCTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAGACATATAACAAAGACCT	1640
Qy	1744	AACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATATTATTAATAAATAAGAGTTTG	1803
Db	1641	AACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATATTATTAATAAATAAGAGTTTG	1700
Qy	1804	CATAACCATCAAAA	1817
Db	1701	CATTACCCCTCAAAA	1714

RESULT 23

ABX16726
ID ABX16726 standard; cDNA; 1732 BP.

AC ABX16726;

AA
DT 03-FEB-2003 (first entry)

DE Human cDNA encoding secreted/transmembrane protein #141.

Human; ss; gene; secreted and transmembrane protein; blood;
tumour necrosis factor-alpha; chondrocyte cell proliferation;
chondrocyte cell differentiation; tumour; adrenal tumour; lung tumour;
colon tumour; breast tumour; prostate tumour; rectal tumour;
cervical tumour; liver tumour; bone disorder; cartilage disorder;
arthritis; sports injury.

XX
OS Homo sapiens.

AA
PN
US2002127584-A1.

12-SEP-2002.
PD

15-JAN-2002: 2002US-0052586.

XX
PR 16-SEP-1998: 98WO-US19330.

PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.

PR 06-JAN-1999; 2000WO-US00219.
PR 08-MAR-1999; 99WO-US05028

PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252

PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090

PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28551

PR 30-DEC-1999; 99WO-US31274.
PR 18-FEB-2000; 2000WO-US04341

PR 18-FEB-2000; 2000WO-US04342.
 PP 23-FEB-2000; 2000WO-US04414

PR 24-FEB-2000; 2000WO-US05004.
BB 01-MAR-2000; 2000WO-US05001

PR 02-MAR-2000; 2000WO-US05841.

WPI; 2003-066893/06.
P-PSDB; ABU10850.

Novel isolated PRO polypeptides e.g., PRO1079, PRO827, PRO791, PRO1131, PRO1316, PRO1183, PRO1343, PRO1760, PRO1567 or PRO4333, useful for stimulating release of tumor necrosis factor-alpha from human blood -

Claim 2; Fig 281; 701pp; English.

The invention relates to an isolated PRO polypeptide comprising at least 80% sequence identity to the protein sequences appearing as ABU10510-ABU10814 (including a version lacking its associated signal peptide, or an isolated extracellular domain of a PRO polypeptide with or without its associated signal peptide. Also included are the nucleic acids encoding the PRO proteins (being secreted and transmembrane proteins) appearing as ABX16586-ABX16590, PRO expression vectors, host cells, chimeric PRO fusion proteins, an anti-PRO antibody and a PRO derived oligonucleotide sequence. The PRO polypeptides are useful for stimulating release of tumor necrosis factor-alpha from human blood. The PRO polypeptide PRO6029 is useful for stimulating proliferation or differentiation of chondrocyte cells. The PRO polypeptides as specified in the specification and having differential expression in tumour cells, are useful for detecting presence of tumour in a mammal (such as adrenal tumour, lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour, cervical tumour or liver tumour. The PRO polypeptide PRO6029 is useful for treating various bone and/or cartilage disorders such as arthritis, and sports injuries. The PRO polypeptides are useful for screening compounds to identify ant/agonists. PRO nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, in the generation of anti-sense RNA and DNA, for the preparation of PRO polypeptides and for generating knock-out animals. The present sequence encodes a PRO polypeptide.

Sequence 1732 BP; 369 A; 592 C; 425 G; 346 T; 0 other;

Query Match	Best Local Similarity	Score	DB	Length	1732;
Matches	Conservative				
424	TTGGGCTGGAGCCTCTCTGGGACTAATGCGACTGTTGGTTCCTCCCTGGACTCCGAGCTCGAGCGCCGCCAGCATGT	483			
321	TGGGACTCGCGTGTCTGTGTTCCCTGGACTCCGAGCTCGAGCGCCGCCAGCATGT	380			
484	TCTGCTTTTCCATGGGAGAGATATCTCCCGCGAGAGCTGCGACCCCTACTTTGGAGC	543			
381	TCTGCTTTTCCATGGGAGAGATATCTCCCGCGAGAGCTGCGACCCCTACTTTGGAGC	440			
544	CACAGGCTGTATGTACTGCTGGCTGTACCTCTCAGAGGGCGCCCATGTGAGTTGTT	603			
441	CACAGGCTGTATGTACTGCTGGCTGTACCTCTCAGAGGGCGCCCATGTGAGTTGTT	500			
604	ACCGCTTCACTGTCCGCTGTCCACTGCTCCAGCTGCGAGCGCCCATGTGAGTTGTT	663			
501	ACCGCTTCACTGTCCGCTGTCCACTGCTCCAGCTGCGAGCGCCCATGTGAGTTGTT	560			
664	GTCCCAAGTGTGGAACCTCACACTCCCTCTGGAAGCTCGGCGCCCATGTGAGTTGTT	723			
561	GTCCCAAGTGTGGAACCTCACACTCCCTCTGGAAGCTCGGCGCCCATGTGAGTTGTT	620			
724	AGCACAAAGGACCATGTACCAACACGAGAGATCTTCACTGCTCCCATGAGCTTCCCT	783			
621	AGCACAAAGGACCATGTACCAACACGAGAGATCTTCACTGCTCCCATGAGCTTCCCT	680			
784	CCCGCTTCCCAACACGAGTGTCTCTGAGCTGCGAGCGCCCATGTGAGTTGTT	843			
681	CCCGCTTCCCAACACGAGTGTCTCTGAGCTGCGAGCGCCCATGTGAGTTGTT	740			
844	TCACAACTGCTCCCAACACGAGTGTCTCTGAGCTGCGAGCGCCCATGTGAGTTGTT	903			
741	TCACAACTGCTCCCAACACGAGTGTCTCTGAGCTGCGAGCGCCCATGTGAGTTGTT	800			
904	AAGCTGTCAAGATGAGGCAAGTGGCAATCGGATCAAGAGGACAGTGTGAGTTGTT	963			

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SQ

15-MAR-2000; 2000WO-US06884.
30-MAR-2000; 2000WO-US08439.
17-MAY-2000; 2000WO-US13705.
22-MAY-2000; 2000WO-US14042.
30-MAY-2000; 2000WO-US14941.
02-JUN-2000; 2000WO-US15264.
28-JUL-2000; 2000WO-US20710.
24-AUG-2000; 2000WO-US23328.
08-NOV-2000; 2000WO-US30952.
01-DEC-2000; 2000WO-US32678.
20-DEC-2000; 2000WO-US34956.
28-FEB-2001; 2001WO-US06520.
01-JUN-2001; 2001WO-US17800.
20-JUN-2001; 2001WO-US19692.
29-JUN-2001; 2001WO-US21066.
09-JUL-2001; 2001WO-US21735.
29-AUG-2001; 2001WO-US27099.
18-SEP-1997; 97US-059263P.
18-SEP-1997; 97US-059266P.
17-OCT-1997; 97US-062250P.
21-OCT-1997; 97US-063486P.
24-OCT-1997; 97US-063120P.
24-OCT-1997; 97US-063121P.
28-OCT-1997; 97US-063540P.
28-OCT-1997; 97US-063541P.
28-OCT-1997; 97US-063544P.
28-OCT-1997; 97US-063564P.
29-OCT-1997; 97US-063734P.
31-OCT-1997; 97US-063870P.
31-OCT-1997; 97US-064103P.
13-NOV-1997; 97US-065311P.
21-NOV-1997; 97US-066120P.
24-NOV-1997; 97US-066466P.
24-NOV-1997; 97US-066772P.
11-DEC-1997; 97US-069335P.
12-DEC-1997; 97US-069425P.
17-DEC-1997; 97US-069870P.
18-DEC-1997; 97US-068017P.
10-MAR-1998; 98US-077450P.
11-MAR-1998; 98US-077632P.
11-MAR-1998; 98US-077649P.
20-MAR-1998; 98US-078886P.
20-MAR-1998; 98US-078939P.
27-MAR-1998; 98US-079664P.
27-MAR-1998; 98US-079786P.
31-MAR-1998; 98US-080107P.
31-MAR-1998; 98US-080194P.
01-APR-1998; 98US-080327P.
01-APR-1998; 98US-080333P.
08-APR-1998; 98US-081049P.
08-APR-1998; 98US-081070P.
09-APR-1998; 98US-081195P.
15-APR-1998; 98US-081838P.
21-APR-1998; 98US-082568P.
21-APR-1998; 98US-082569P.
22-APR-1998; 98US-082704P.
22-APR-1998; 98US-082797P.
28-APR-1998; 98US-083222P.
29-APR-1998; 98US-083495P.
29-APR-1998; 98US-083496P.
29-APR-1998; 98US-083499P.
29-APR-1998; 98US-083559P.
05-MAY-1998; 98US-084366P.
06-MAY-1998; 98US-084414P.
07-MAY-1998; 98US-084639P.
07-MAY-1998; 98US-084640P.
07-MAY-1998; 98US-084643P.

(GETH) GENENTECH INC.
Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

QY	424	TTGGGCTGGAGCCTCCTCGGACTTAACATGGCACTGGTCGGTTTGCCAGGCGCCAGACATGT	483
Db	341	TGGGACTCGCGTGCTCTGGTTCCCTCGACTCCACGCTCGAGCCCGCCAGACATGT	400
QY	484	TCTCCCTTTTCCATGGGAAGAGATATCCCCCGGCGAGAGCTGSCACCCCTACTTGGAGC	543
Db	401	TCTGCCCTTTCCATGGGAAGAGATATCCCCCGGCGAGAGCTGSCACCCCTACTTGGAGC	460
QY	544	CACAAGGCTGATGTACTGCTGCGGTGTACTTGCTCAGAGGGGCCCATGTGAGTTGTT	603
Db	461	CACAAGGCTGATGTACTGCTGCGGTGTACTTGCTCAGAGGGGCCCATGTGAGTTGTT	520
QY	604	ACCGGCTTCACTGTTCGGCTGTTCCTGCTGCCCCGAGCTGTGACGGAGGCCACAGCAATGCT	663
Db	521	ACCGGCTTCACTGTTCGGCTGTTCCTGCTGCCCCGAGCTGTGACGGAGGCCACAGCAATGCT	580
QY	664	GTCCCAAGTGTGTGAACCTCAACATCCCTCTGGACTCCGGGCCCCACCAAGTCCCTGCC	723
Db	581	GTCCCAAGTGTGTGAACCTCAACATCCCTCTGGACTCCGGGCCCCACCAAGTCCCTGCC	640
QY	724	AGCACACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCT	783
Db	641	AGCACACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCT	700
QY	784	CCCGCTCCCAACCAAGTGTCTCTGCACTGTGCAAGAGGGGCGAGTCTACTGCGGCC	843
Db	701	CCCGCTCCCAACCAAGTGTCTCTGCACTGTGCAAGAGGGGCGAGTCTACTGCGGCC	760
QY	844	TCACAACCTGCCCGCGAACAAGGTGCCAGACACCCCTCCCGCTGCCAGACTCTCTGCTGCC	903
Db	761	TCACAACCTGCCCGCGAACAAGGTGCCAGACACCCCTCCCGCTGCCAGACTCTCTGCTGCC	820
QY	904	AAGCCTGCAAGATGAGGCAAGTGAGCAATCGGATGAAGAGAGCAAGTGTGAGTCGCTCC	963
Db	821	AAGCCTGCAAGATGAGGCAAGTGAGCAATCGGATGAAGAGAGCAAGTGTGAGTCGCTCC	880
QY	964	ATGGGTTGAGACATCCTCAGGATCCATGTTTCCAGTGATGCTGGGAGAAGAGAGCCCG	1023
Db	881	ATGGGTTGAGACATCCTCAGGATCCATGTTTCCAGTGATGCTGGGAGAAGAGAGCCCG	940
QY	1024	GCACCCAGCCCCCACTGGGCTCAGCGCCCTCTGAGTTCATCCCTCGCCAATTGAGAC	1083
Db	941	GCACCCAGCCCCCACTGGGCTCAGCGCCCTCTGAGTTCATCCCTCGCCAATTGAGAC	1000
QY	1084	CCAAGGAGCAGCAGCACAACTGTCAAGATCGTCTGAAGAGAGAAACATAGAAAGCCT	1143
Db	1001	CCAAGGAGCAGCAGCACAACTGTCAAGATCGTCTGAAGAGAGAAACATAGAAAGCCT	1060
QY	1144	GTGTGCATGGCGGGAAGACGTACTCCACGGGAGGTGTGGCACCCCGCTTCCTCGTGCCCT	1203
Db	1061	GTGTGCATGGCGGGAAGACGTACTCCACGGGAGGTGTGGCACCCCGCTTCCTCGTGCCCT	1120
QY	1204	TCGGCCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCGCAGGACTGCCACGCTG	1263
Db	1121	TCGGCCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCGCAGGACTGCCACGCTG	1180
QY	1264	TGACCTGTCCACCGAGTACCCCTTCGCGTCAACCCCGAGAAAGTGGCTGGGAAAGTGTGCA	1323
Db	1181	TGACCTGTCCACCGAGTACCCCTTCGCGTCAACCCCGAGAAAGTGGCTGGGAAAGTGTGCA	1240
QY	1324	AGATTTTCCAGAGGACAAAGACAGACCCCTGGCCACAGTGAGATCAGTTCTTCCAGGTGTC	1383

R P-PSDB; AAB68077.

Nucleic acids encoding splice variants of a chordin like homolog, useful in the treatment of bone injuries, diseases involved with the female reproductive tract, diseases involving sexual hormone abnormalities and cardiovascular disorders.

Claim 1; Page 180-181; 203pp; English.

The present sequence encodes a splice variant of a chordin like homologue (CLH). The protein is a homologue to the known chordin within the von-Willebrand factor type C (VWFC) domain repeat, which is found 2-4 times in these multi-domain proteins. The present protein contains 3 VWFC repeats. CLH proteins and polynucleotides can be used for the treatment of diseases which can be ameliorated, cured or prevented by raising the level of a CLH. The nucleic acids, expression vectors, proteins and antibodies are useful in the treatment of a disease selected from diseases manifested in non-normal bone formation and non-normal bone modelling, bone injuries, diseases involved with the female reproductive tract, diseases of disorders involved with abnormal sexual differentiation, recurrent miscarriages, tumours of the uterus, breast or prostate, diseases involving sexual hormone abnormalities, cardiovascular disorders, neuronal diseases of the CNS (central nervous system), or neurodegenerative diseases and diseases involving non-normal developments of neurons.

Sequence 1722 BP; 351 A; 594 C; 425 G; 352 T; 0 other;

Query Match	73.6%	Score 138;	DB 22;	Length 1722;
Best Local Similarity	97.5%;			
Matches 135;	Conservative	0;	Pred. NO. 0;	
Mismatches	35;	Indels	0;	Caps 0;

424	TTGGGCTGGAGCCTCTCGGGACTAACATGGCACTGGTTCGGTTTGCAGGCCACAGACATGT	483
329	TGGGACTCGCGCTGCTGTGTTCCCTCTGACTCCACGCTCGAGCCGCGCCAGACATGT	388
484	TCCTGCCTTTTCCATGGGAAGAGATACTCCCGCGGAGAGCTGGCAACCCCTACTCTGGAGC	543
389	TCCTGCCTTTTCCATGGGAAGAGATACTCCCGCGGAGAGCTGGCAACCCCTACTCTGGAGC	448
544	CACAAGGCCCTGATGTACTGCCTGGCGTGTAACCTGCTCAGAGGGCGCCCATGTGAGTTGTT	603
449	CACAAGGCCCTGATGTACTGCCTGGCGTGTAACCTGCTCAGAGGGCGCCCATGTGAGTTGTT	508
604	ACGGCCTTCGACTGTCCGCTGTGTCCACTGCCCGCCAGCCTGTGTGACGGAGCCACAGCAATGCT	663
509	ACGGCCTTCGACTGTCCGCTGTGTCCACTGCCCGCCAGCCTGTGTGACGGAGCCACAGCAATGCT	568
664	GTCCCAAGTGCTGTGGAACTTACACTCCCTCTGGACTCCGGGCCCCACAAAGTCTCTGCC	723
569	GTCCCAAGTGCTGTGGAACTTACACTCCCTCTGGACTCCGGGCCCCACAAAGTCTCTGCC	628
724	AGCACAACGGGACCATATGACACAACGGAGAGATCTTCACTGCCCATGAGCTGTTCCTCCT	783
629	AGCACAACGGGACCATATGACACAACGGAGAGATCTTCACTGCCCATGAGCTGTTCCTCCT	688
784	CCGCGCTGCCCAACCACTGTCTCTGACAGTGCACAGAGGGCCAGATCTACTCGGGCC	843
689	CCGCGCTGCCCAACCACTGTCTCTGACAGTGCACAGAGGGCCAGATCTACTCGGGCC	748
844	TCACAACCTGCCCGAACACAGGCTGCCAGACACCCCTCCCGTGCACAGCTCCTGTGCTCC	903
749	TCACAACCTGCCCGAACACAGGCTGCCAGACACCCCTCCCGTGCACAGCTCCTGTGCTCC	808
904	AAGCCTGCAAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGACAAGTGTGCACTGCTCTCC	963
809	AGGCCTGCAAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGACAAGTGTGCACTGCTCTCC	868
964	ATGGGGTGAGACATCCTCAGGATCCATGTTTCCAGTGTGCTGGGAGAAAGAGAGGCCCGG	1023
869	ATGGGGTGAGACATCCTCAGGATCCATGTTTCCAGTGTGCTGGGAGAAAGAGAGGCCCGG	928
1024	GCACCCCGAGCCCCACCTGGCCTCAGCGCCCCCTCTGAGCTTTCATCCCTCGCCACTTCAGAC	1083

929	DB	GCACCCAGCCCCACTGGCCTCAGCGCCCTCTGAGCTTCATCCTCGCCACTTCATAC	988
1084	QY	CCAAAGGAGCGGACGACCAACTGTCAGATCGTCTGAGAGAGAAACATAGAAGCCT	1143
989	DB	CCAAAGGAGCGGACGACCAACTGTCAGATCGTCTGAGAGAGAAACATAGAAGCCT	1048
1144	QY	GTGTGCATGGCGGGAAGCGTACTCCACGGGAGGTGGGCACCGGCGCTTCGGTGCCT	1203
1049	DB	GTGTGCATGGCGGGAAGCGTACTCCACGGGAGGTGGGCACCGGCGCTTCGGTGCCT	1108
1204	QY	TCGGCCCCCTTGCCCTGCATCTTATGCACCTGTGAGGATGGCCGCCAGAGACTGCCAGCTG	1263
1109	DB	TCGGCCCCCTTGCCCTGCATCTTATGCACCTGTGAGGATGGCCGCCAGAGACTGCCAGCTG	1168
1264	QY	TGACCTGTCCCAACGAGTACCCCTGCGTCACCCCGAGAAAGTGGGTGGAGTGTCTGCA	1323
1169	DB	TGACCTGTCCCAACGAGTACCCCTGCGTCACCCCGAGAAAGTGGGTGGAGTGTCTGCA	1228
1324	QY	AGATTTGGCCACGAGGACAAAGCAGACCCCTGGGCCACAGTGAGATCAGTTCTACACAGGTGC	1383
1229	DB	AGATTTGGCCACGAGGACAAAGCAGACCCCTGGGCCACAGTGAGATCAGTTCTACACAGGTGC	1288
1384	QY	CCAAGGCCACCGGCGCGGTCCTCGTCCACACATCGGTATCCCAAGCCAGACAACCTGC	1443
1289	DB	CCAAGGCCACCGGCGCGGTCCTCGTCCACACATCGGTATCCCAAGCCAGACAACCTGC	1348
1444	QY	GTGCGTTTGGCCCTGGAAACGAGGCGCTCGGACTTGGTGAGATCTACCTCTGGAAGCTGG	1503
1349	DB	GTGCGTTTGGCCCTGGAAACGAGGCGCTCGGACTTGGTGAGATCTACCTCTGGAAGCTGG	1408
1504	QY	TAAAGATGAGGAAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCC	1563
1409	DB	TAAAGATGAGGAAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCC	1468
1564	QY	AGAATCTTCCACTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGGCCA	1623
1469	DB	AGAATCTTCCACTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGGCCA	1528
1624	QY	CAGCACTTCCGACTGCTGCTGGCCCCACGAAAGTCACTGAAACGTCTCTTAGCCCCAG	1683
1529	DB	CAGCACTTCCGACTGCTGCTGGCCCCACGAAAGTCACTGAAACGTCTCTTAGCCCCAG	1588
1684	QY	ACCTTGGAGCTGAAGGTCAAGGCTCAGGCGCAGTCCAGACAAAGTGACCAAGACATAACAAAGCCT	1743
1589	DB	ACCTTGGAGCTGAAGGTCAAGGCTCAGGCGCAGTCCAGACAAAGTGACCAAGACATAACAAAGCCT	1648
1744	QY	AAACAGTTCAGATATGAGCTGTATAATTGTTGTTATTATATTAAATAAGAGTTG	1803
1649	DB	AAACAGTTCAGATATGAGCTGTATAATTGTTGTTATTATATTAAATAAGAGTTG	1708
1804	QY	CATAACCATCAAAA	1817
1709	DB	CATAACCATCAAAA	1722

RESULT 26

AAE84771
ID AAE84771 standard: DNA: 1722 bp.

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DT 09-JUL-2001 (first entry)

XX
DE
f. 100
1000

DE Nucleotide sequence of a human chordin-like homologue splice variant.

XX Splice variant; chordin like homologue; CUIH; bone modelling; bone injury;
KW von-Willebrand factor type C repeat; VWF repeat; bone formation;
KW reproductive disease; sexual differentiation; miscarriage; tumour;
KW sexual hormone; cardiovascular disorder; neuronal disease;
KW neurodegenerative disease; neuron development; ss.

xx Homo sapiens.

570 GTCCCAAGTGTGTGGAAACCTTCACACTCCCTCTGGAGATCCCGGGCCCCACCAAGTCTCTGCC 629

724 AGCACAACGGGACCATGTATCCACACGGAGAGATCTTTCAGTGCCCATCAGAGTGTTCCTCCCT 783

630 AGCACAACGGGACCATGTATCCACACGGAGAGATCTTTCAGTGCCCATCAGAGTGTTCCTCCCT 689

784 CCGCCCTGCCCAACCAAGTGTGTCTCTGCACTGTGCACAGAGGGCCAGATCTACTCTGCGGCC 843

690 CCGCCCTGCCCAACCAAGTGTGTCTCTGCACTGTGCACAGAGGGCCAGATCTACTCTGCGGCC 749

844 TCACAACCTGCCCCCGAAACCAAGGTGCCAGCACCCCTCCCGCTGCCAGACTCTCTGCTGCC 903

750 TCACAACCTGCCCGAAACCAAGGTGCCAGCACCCCTCCCGCTGCCAGACTCTCTGCTGCC 809

904 AAGCTGTCAAGAATGAGGCAAGTGAGCAATCCGATGAAGAGGACAGTGTGCAGTGCCTCC 963

810 AAGCTGTCAAGAATGAGGCAAGTGAGCAATCCGATGAAGAGGACAGTGTGCAGTGCCTCC 869

964 ATGGGGTGAACATCTCTCAGGATCCATGTTCCAGTGTCTGGGAGAAAGAGAGGCCCGG 1023

870 ATGGGGTGAACATCTCTCAGGATCCATGTTCCAGTGTCTGGGAGAAAGAGAGGCCCGG 929

1024 GCACCCAGCCCCCACTGGGCTCAGGGCCCTCTGAGCTTCACTCCCTGCCACTTCAGAC 1083

930 GCACCCAGCCCCCACTGGGCTCAGGGCCCTCTGAGCTTCACTCCCTGCCACTTCAGAC 989

1084 CCAAGGAGCAGGACGACAACTCTCAAGATCTGCTCAAGGAGGAGAAACATAAGAAAGCCT 1143

990 CCAAGGAGCAGGACGACAACTCTCAAGATCTGCTCAAGATCTGCTCAAGGAGGAGAAACATAAGAAAGCCT 1049

1144 GTGTGATGCGGGGAAAGACGTACTCCACCGGGGAGGTGTGGCACCCGGCTTCCTCGTGCCT 1203

1050 GTGTGATGCGGGGAAAGACGTACTCCACCGGGGAGGTGTGGCACCCGGCTTCCTCGTGCCT 1109

1220 TCGGCCCCCTTGCCCTGCATCTCTATGCACCTGTAGGATGTGGCGCCGACAGACTGCCACGCTG 1263

1110 TCGGCCCCCTTGCCCTGCATCTCTATGCACCTGTAGGATGTGGCGCCGACAGACTGCCACGCTG 1169

1264 TGACTGTCCACCGAGTATACCTCGCTCACCCCGAGAAAGTGGCTGGGAAGTGTCTGCA 1323

11170 TGACTGTCCACGAAATGATCCCTCGCTCACCCCGAAAGTGGCTGGGAAGTGTCTGCA 1329

1324 AGATTTGCCAGAGGACAAAGACAGACCCTGGCCACAGTGAGATCAGTTCTTACCAAGTGTCT 1383

1230 AGATTTGCCAGAGGACAAAGACAGACCCTGGCCACAGTGAGATCAGTTCTTACCAAGTGTCT 1289

1384 CCAAGGACCCGGGCGGGTCTCTGTCACACATCGGTATCCCAAGCCCAAGCCAGCAACTGTC 1443

1290 CCAAGGACCCGGGCGGGTCTCTGTCACACATCGGTATCCCAAGCCCAAGCCAGCAACTGTC 1349

1444 GTGCTTTGCCCTGGAAACAGAGGCTCGACTTGGTGGAGATCTACCTCTGGAAGCTGG 1503

1350 GTGCTTTGCCCTGGAAACAGAGGCTCGACTTGGTGGAGATCTACCTCTGGAAGCTGG 1409

1504 TAAAGATGAGGAAACTGAGGCTCAGAGAGGTGAAGTACTCGGCCCAAGGCCACACAGCC 1563

1410 TAAAGATGAGGAAACTGAGGCTCAGAGAGGTGAAGTACTCGGCCCAAGGCCACACAGCC 1469

1564 AGAATCTTTCCACTTGACTCAGATCAAGAAGTGTGAGGACCAAGACTTCCAGAAAGAGGCA 1623

1470 AGAAT-TTCCACTTGACTCAGATCAAGAAGTGTGAGGACCAAGACTTCCAGAAAGAGGCA 1528

1624 CAGCACTTCGAGCTGCTCGCTGGCCCCCAGAAAGTCACTGNAACCTCTCTTAGCCAG 1683

1529 CAGCACTTCGAGCTGCTCGCTGGCCCCCAGAAAGTCACTGGAACCTCTCTTAGCCAG 1588

1684 ACCCTGGAGCTGAAGGTCAAGGCTCAGCCAGTCCAGACAAAGTGCACCAAGACATAAACAAAGACCT 1743

1589 ACCCTGGAGCTGAAGGTCAAGGCTCAGCCAGTCCAGACAAAGTGCACCAAGACATTAACCAAGACCT 1648

1744 AACAGTTCAGATATGAGCTGTATTAATCTGTGTTATTAATTAATTAATAAGAAAGTGT 1803

1649 AACAGTTCAGATATGAGCTGTATTAATCTGTGTTATTAATTAATTAATAAGAAAGTGT 1708

y	904	AAGCCTGCAAGAATGAGGC	AAAGTGAACAATCGAATGAAGAGGACAGTGTCAGTCGTCC	963
b	515	ARGCCTGCAAAGATGAGG	CAAGTGAACAATCGAATGAAGAGGACAGTGTCAGTCGTCC	574
y	964	ATGGGTTGAGACATCCT	CAGGATCCAATGTTCCAGTGCATGCTGGAGAAACAGAGGCCCGG	1023
b	575	ATGGGTTGAGACATCCT	CAGGATCCAATGTTCCAGTGCATGCTGGAGAAACAGAGGCCCGG	634
y	1024	GCACCCCAGCCCCCAT	GCGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC	1083
b	635	GCACCCCAGCCCCCAT	GCGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC	694
y	1084	CCAGGGAGCAGGACGAC	CAACTGTCAAGATCGTCTGAAGAGAAACATAAGAAAGCCT	1143
b	695	CCAAAGGAGCAGGACG	ACAACTGTCAAGATCGTCTGAAGAGAAACATAAGAAAGCCT	754
y	1144	GTGTGCATGGCGGGAAG	TACTCCACGGGAGGTGTGGCACCCCGCCCTTCGTGTCCT	1203
b	755	GTGTGCATGGCGGGAAG	TACTCCACGGGAGGTGTGGCACCCCGCCCTTCGTGTCCT	814
y	1204	TCGGCCCCCTTGCCCT	GTGCATCTATGACCTGTGAGATGGCCCCCAGGACTGCCAGCGTG	1263
b	815	TCGGCCCCCTTGCCCT	GTGCATCTATGACCTGTGAGATGGCCCCCAGGACTGCCAGCGTG	874
y	1264	TGACCTGTCCACCGAG	TACCCTGCCGTCAACCCGAGAAAGTGGCTGGAAAGTGTGCA	1323
b	875	TGACCTGTCCACCGAG	TACCCTGCCGTCAACCCGAGAAAGTGGCTGGAAAGTGTGCA	934
y	1324	AGATTGCCCCAGAGACA	AGAACAGACCCCTGGCCACAGTGAGATCAGTCTTACACAGGTGTC	1383
b	935	AGATTGCCCCAGAGACA	AGAACAGACCCCTGGCCACAGTGAGATCAGTCTTACACAGGTGTC	994
y	1384	CAAAGGCACCGGGCCG	GTCTTCGCACACATCGGTATCCCCAAGCCCCAGACAACCTGC	1443
b	995	CAAAGGCACCGGGCCG	GTCTTCGCACACATCGGTATCCCCAAGCCCCAGACAACCTGC	1054
y	1444	GTGCTTTGCCCTTGGAA	CACGAGGCTCGGACTTGGTGAGATCTACTCTTGGAAAGCTGG	1503
b	1055	GTGCTTTGCCCTTGGAA	CACGAGGCTCGGACTTGGTGAGATCTACTCTTGGAAAGCTGG	1114
y	1504	TAAAGATGAGGAAACT	GAGGCTCAGAGAGGTGAAGTACTTGGCCCCAAGGCCACACAGCC	1563
b	1115	TAAAGATGAGGAAACT	GAGGCTCAGAGAGGTGAAGTACTTGGCCCCAAGGCCACACAGCC	1174
y	1564	AGAATCTTCCACTTGAC	TTCAGATCAAGAAGTCAGGAACAGACTTCCAGAAGAGGCA	1623
b	1175	AGAATCTTCCACTTGAC	TTCAGATCAAGAAGTCAGGAACAGACTTCCAGAAGAGGCA	1234
y	1624	CAGCACTTCCGACTGCT	CGCTGGCCCCCAGAAAGTCACTTGGAAAGCTCTTCTTAGGCCAG	1683
b	1235	CAGCACTTCCGACTGCT	CGCTGGCCCCCAGAAAGTCACTTGGAAAGCTCTTCTTAGGCCAG	1294
y	1684	ACCTTGGAGCTGAAGGT	CAGGCCAGTCCAGACAAAGTGACCAAGACATTAACAAAAGCCT	1743
b	1295	ACCTTGGAGCTGAAGGT	CAGGCCAGTCCAGACAAAGTGACCAAGACATTAACAAAAGCCT	1354
y	1744	AA	1745	
b	1355	AA	1356	

ESULT 29
AS84494
D - AAS84494 standard; cDNA; 1497 BP.
X AAS84494;

RESULT	29
AS84494	
D	AAS84494 standard; cDNA; 1497 BP.
X	
C	AAS84494;

13-FEB-2002 (first entry)

3 DNA encoding novel human diagnostic protein #20298.

X Human; chromosome mapping; gene mapping; gene therapy; forensic;
W food supplement; medical imaging; diagnostic; genetic disorder; ss.
M Human; chromosome mapping; gene mapping; gene therapy; forensic;
W food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.
OS
XX
XX WO200175067-A2.
PN
XX
XX 11-OCT-2001.
PD
XX
XX 30-MAR-2001; 2001WO-US086311.
XX
XX 31-MAR-2000; 2000US-0540217.
PR
XX 23-AUG-2000; 2000US-0649167.
PR
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
PI
XX
XX WPI; 2001-639362/73.
DR P-PSDB; ABG20307.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX Claim 1; SEQ ID NO 20298; 103pp; English.
PS
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polynucleotide chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 1497 BP; 360 A; 475 C; 387 G; 275 T; 0 other;
SQ

Query Match	69.2%	Score 1257	DB 23	Length 1497
Best Local Similarity	97.9%	Pred. No. 0		
Matches 1328	Conservative	0	Mismatches 20	Indels 9
				Gaps 5

QY	470	AGGCCCAGACATGTTCTGCTCTTTTCCATGGGAGAGATACTCCCCCGGCGAGAGCTGGCA	529
Db	136	ATGCCCAGACATGTTCTGCTCTTTTTCATGGGAGAGATACTCCCCCGGCGAGAGCTGGCA	195
QY	530	CCCTACTTTGGAGCCACAAGGCGCTGATGTACTGCCTGCGCTGTACTGCTCAGAGGGCGC	589
Db	196	CCCTACTTTGGAGCCACAAGGCGCTGATGTACTGCCTGCGCTGTACTGCTCAGAGGGCGC	255
QY	590	CCATGTGAGTTGTTACCGGCTCCACTGTGCGGCTGTCCACTGCCCCCAGCGCTGTGACGGA	649
Db	256	CCATGTGAGTTGTTACCGGCTCCACTGTGCGGCTGTCCACTGTCCTCCAGCGCTGTGACGGA	315
QY	650	GCACACAGCAATGCTGTCCAAAGTGTGGAAACCTCACACTCCCTCTTGGAATCTCGGGGGCCC	709
Db	316	GCACACAGCAATGCTGTCTCCAAAGTGTGGAAACCTCACACTCCCTCTTGGAATCTCGGGGGCCC	375
QY	710	ACCAAGTCCTGCCAGCAACAACGGGACCAATGTACCAACACGGAGAGATCTTCAGTGGCCCA	769
Db	376	ACCAAGTCCTGCCAGCAACAACGGGACCAATGTACCAACACGGAGAGATCTTCAGTGGCCCA	435

RESULT_30

AAF84770
ID AAF84770 standard; DNA; 1281 BP.

XX
AC AC
XX AAF84770;

XX
DT 09-JUL-2001 (first entry)

XX
DE Nucleotide sequence of a human chordin-like homologue.

XX
KW Splice variant; chordin like homologue; CLH; bone modelling; bone injury;
KW von-Willebrand factor type C repeat; VWFC repeat; bone formation;
KW reproductive disease; sexual differentiation; miscarriage; tumour;
KW sexual hormone; cardiovascular disorder; neuronal disease;
KW neurodegenerative disease; neuron development; ss.
XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT CDS 2..1198
FT FT /*tag= a
FT FT /transl_except= "(pos: 599..601, aa: Xaa)"
FT FT /product= "chordin-like homologue"
FT FT /note= "Xaa represents an unspecified amino acid"

XX
PN WO200134796-A1.

XX
PD 17-MAY-2001.

XX
PF 10-NOV-2000; 2000WO-IL00736.

XX
PR 10-NOV-1999; 99IL-0132846.
PR 28-DEC-1999; 99IL-0133767.

XX
PA (COMP-) COMPUGEN LTD.

XX
PI Toporok A, Biton S, Savitzky K, Bernstein J;
XX WPI; 2001-308783/32.
DR P-PSDB; AAB68073.

XX
PT Nucleic acids encoding splice variants of a chordin like homolog,
PT useful in the treatment of bone injuries, diseases involved with the
PT female reproductive tract, diseases involving sexual hormone
PT abnormalities and cardiovascular disorders -
XX Claim 1; Page 178; 203pp; English.

XX
CC The present sequence encodes a chordin like homologue (CLH). The protein
CC is a homologue to the known chordins within the von-Willebrand factor
CC type C (VWFC) domain repeat, which is found 2-4 times in these
CC multi-domain proteins. CLH proteins and polynucleotides can be used for
CC the treatment of diseases which can be ameliorated, cured or prevented by
CC raising the level of a CLH. The nucleic acids, expression vectors,
CC proteins and antibodies are useful in the treatment of a disease selected
CC from diseases manifested in non-normal bone formation and non-normal bone
CC modelling, bone injuries, diseases involved with the female reproductive
CC tract, diseases of disorders involved with abnormal sexual
CC differentiation, recurrent miscarriages, tumours of the uterus, breast
CC or prostate, diseases involving sexual hormone abnormalities,
CC cardiovascular disorders, neuronal diseases of the CNS (central nervous
CC system), or neurodegenerative diseases and diseases involving non-normal
CC developments of neurons.

XX
SQ Sequence 1281 BP; 313 A; 405 C; 335 G; 227 T; 1 other;

Query Match 69.1%; Score 1256.4; DB 22; Length 1281;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1271; Conservative 0; Mismatches 7; Indels 1; Gaps 1

OY 539 GGAGGCCAAGCGCTGATGTACTGCCTGGCTGTACTGTCTCAGAGGCGCCCATGTGAG 598

4	GGAGCCACAAGCCCTGATGTACTGCTGCGCTGTACTCTGTCAGAGGGGCGCCATGTGAG	63
599	TTGTTACCGCCTCCACTGTCCGGCTGTCCACTGCGCCCGCCAGCCTGTGACGAGGCCACAGCA	658
64	TTGTTACCGCCTCCACTGTCCGGCTGTCCACTGCGCCCGCCAGCCTGTGACGAGGCCACAGCA	123
659	ATGCTGTCCCAAAGTGTGTGGAACTCACACTCCCTCTGGACTCCGGGCCCCACCAAGTC	718
124	ATGCTGTCCCAAAGTGTGTGGAACTCACACTCCCTCTGGACTCCGGGCCCCACCAAGTC	183
719	CTGCAGACAAACGGGACCATGTATCCAAACGAGAGATCTTCAGTGCCTCATGAGCTGTT	778
184	CTGCAGACAAACGGGACCATGTATCCAAACGAGAGATCTTCAGTGCCTCATGAGCTGTT	243
779	CCCTCCCGCCTGCCCAACCAAGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTTACTG	838
244	CCCTCCCGCCTGCCCAACCAAGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTTACTG	303
839	CGGCTCTCAACCTGCGCCCGAACCGGCTGCCAGCACCCCTCCCGCTGCACACTCCCTG	898
304	CGGCTCTCAACCTGCGCCCGAACCGGCTGCCAGCACCCCTCCCGCTGCACACTCCCTG	363
899	CTGCCAAGCCTCAAAAGATGAGGCAAGTAGCAATCGGATGAAGAGACAGTGTGCAGTC	958
364	CTGCCAAGCCTCAAAAGATGAGGCAAGTAGCAATCGGATGAAGAGACAGTGTGCAGTC	423
959	GCTCCATGGGTGAGACATCTCTCAGGATCCATGTTCCAGTGTGCTGGGAGAAAGAGAGG	1018
424	GCTCCATGGGTGAGACATCTCTCAGGATCCATGTTCCAGTGTGCTGGGAGAAAGAGAGG	483
1019	CCGGGACCCACAGCCCCCACTGGGCCCTCAGGGCCCTCTGAGTTTCACTCCCTCGCCACTT	1078
484	CCGGGACCCACAGCCCCCACTGGGCCCTCAGGGCCCTCTGAGTTTCACTCCCTCGCCACTT	543
1079	CAGACCCAAGGAGCAGCAGACACACTGTCAAGATCGTCTTGAAGAGAAACATTAAGAA	1138
544	CAGACCCAAGGAGCAGCAGACACACTGTCAAGATCGTCTTGAAGAGAAACATTAAGAA	603
1139	AGCCTGTGTGATGCGGGAGAGAGTACTCCACAGGGGAGGTGTGGCACCCGCGCTTCGG	1198
604	AGCCTGTGTGATGCGGGAGAGAGTACTCCACAGGGGAGGTGTGGCACCCGCGCTTCGG	663
1199	TGCCTTCGCGCCCTTGCCTGTCATCTATGCACCTGTGAGGATGGCGCCAGACTGCACA	1258
664	TGCCTTCGCGCCCTTGCCTGTCATCTATGCACCTGTGAGGATGGCGCCAGACTGCACA	723
1259	CGGTGTACCTTCCCAACGAGTACCCCTGCGCTACCCCGAGAAAGTGGCTGGGAAGTG	1318
724	CGGTGTACCTTCCCAACGAGTACCCCTGCGCTACCCCGAGAAAGTGGCTGGGAAGTG	783
1319	CTGCAAGATTTGCCAGAGGACAAAGAGACCTTGGCCACAGTGTGATCAGTTCTTACCAG	1378
784	CTGCAAGATTTGCCAGAGGACAAAGAGACCTTGGCCACAGTGTGATCAGTTCTTACCAG	843
1379	GTGTCCTCCAAAGCACGGGCGGGTCTCTGTCCACACATCGGTATCCCCAAGCCACACAA	1438
844	GTGTCCTCCAAAGCACGGGCGGGTCTCTGTCCACACATCGGTATCCCCAAGCCACACAA	903
1439	CCTGGCTCGCTTTGCCCTGGAACAGAGGCCCTCGGACTTGTGTGGAGATCTTACTCTGGAA	1498
904	CCTGGCTCGCTTTGCCCTGGAACAGAGGCCCTCGGACTTGTGTGGAGATCTTACTCTGGAA	963
1499	GCTGTTAAAAGATGAGGAAACTGAGGCTCAGAGAGGTGAAGTACCTTGGCCCAAGGCCACA	1558
964	GCTGTTAAAAGATGAGGAAACTGAGGCTCAGAGAGGTGAAGTACCTTGGCCCAAGGCCACA	1023
1559	CAGCCAGAATCTTCCACTTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAG	1618
1024	CAGCCAGAATCTTCCACTTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAG	1082
1619	AGGCAACAGACTTCCGACTGTGCTGCTGGCCCCCACGAAGGTCACTGGAACGCTTCTCTAG	1678
1083	AGGCAACAGACTTCCGACTGTGCTGCTGGCCCCCACGAAGGTCACTGGAACGCTTCTCTAG	1142

RESULT 31

ABK12124

ID ABK12124 standard; cDNA; 1406 BP.

AC ABK12124:

05-JUN-2002 (first entry)

Human cDNA encoding chordin homologue Lp226.

Human: ss: gene: chordin homologue: RP226. n

Aztreonam's disease Parkinson's disease; wound; tissue repair;
bone fracture; spinal cord injury; pressure ulcer; diabetic ulcer;
venous stasis ulcer; burn; cardiovascular disorder; arteriosclerosis;
thrombosis; heart failure; proliferative disorder; osteosarcoma;
breast cancer; leukaemia; prostate cancer; bone mineral density disorder;
osteopaenia-related disorder; fibrotic disorder; cirrhosis;
chronic asbestosis; restenosis; Gaucher's disease; Marfan's disease;
anaemia; diabetes mellitus; osteoporosis; transgenic.

OS Homo sapiens.

Kev

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FT CDS

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W0200208277-2

31-TAN-2002

XX
Ed
05-JUL-2001:XX
19-III-3000.PR 04-MAY-2001;
yy

PA (ELIL) LILLY
yy

PI Alvarez E, M
yy

BR WPI; 2002-280

1000

cysteine-rich

1

Claim 3; Page 7-9; 149pp; English.

The invention relates to isolated LP polypeptides (which have significant sequence similarity to the cysteine-rich regions of chordin being LP226, LP233 and LP236) and encoding polynucleotides. The mature portions of the LP proteins and the region of the nucleic acid encoding them are also included. Also included are a vector comprising the polynucleotide, a host cell comprising the vector, an anti-LP antibody and ant/agonists of the LP proteins. LP is useful in the manufacture of a medicament. LP, LP polynucleotide agonists or antagonists of LP are useful for diagnosis and treatment of a neurological disorder (e.g. Alzheimer's disease and Parkinson's disease), a disorder requiring wound or tissue repair (where the disorder is selected from bone fracture, spinal cord injury, pressure ulcer, diabetic ulcer, venous stasis ulcer, and burn), a cardiovascular disorder (e.g. atherosclerosis, thrombosis and heart failure), a proliferative disorder such as osteosarcoma, breast cancer, leukaemia and prostate cancer, a disorder associated with loss of bone mineral density, an osteopaenia-related disorder, or a fibrotic disorder (e.g. cirrhosis and chronic asbestosis) restenosis, Gaucher's disease, Marfan's disease, anaemia, diabetes mellitus, osteoporosis and many other diseases and disorders listed in the specification. LP is useful for identifying compounds that bind to LP, and to isolate correlative ligands. LP polynucleotide as hybridisation probes, in chromosome and gene mapping, and in the generation of antisense RNA and DNA, for the preparation of LP, for generating either transgenic or knock out animals, and for chromosome identification. The antibody is useful in diagnostic and assays for LP, for affinity purification of LP and as diagnostic and therapeutic agent. The present sequence encodes the LP protein LP226.

Sequence 1406 BP; 323 A; 458 C; 367 G; 258 T; 0 other;

Query Match	67.3%;	Score	1222.8;	DB	24;	Length	1406;	
Best Local Similarity	93.8%;	Pred.	No. 0;					
Matches 1307;	Conservative	0;	Mismatches	32;	Indels	55;	Gaps	1;
QY	424	TTGGGCTGGAGCTCTCGGACCTAATGACGACCTGCTGGTTCAGGCGCCAGACATGT	483					
DB	63	TGGGACTCGCGTGTCTGTGTTCCCTCGGACTCCACGCTCGAGCCGCGCCAGACATGT	122					
QY	484	TCTGCTTTTCCATGGGAGAGATATCTCCCGCGGAGAGCTGGCACCCCTACTTTGGAGC	543					
DB	123	TCTGCTTTTCCATGGGAGAGATATCTCCCGCGGAGAGCTGGCACCCCTACTTTGGAGC	182					
QY	544	CACAAGCCCTGATGTACTGCTGGCTGTACTCTCTCAGAGGGCGCCCATGTGAGTTGTT	603					
DB	183	CACAAGCCCTGATGTACTGCTGGCTGTACTCTCTCAGAGGGCGCCCATGTGAGTTGTT	242					
QY	604	ACGCTCTCCACTGTCCGCTGTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATGCT	663					
DB	243	ACGCTCTCCACTGTCCGCTGTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATGCT	302					
QY	664	GTCCCAAGTGTGGAAACCTCACACTCCCTCTGACTCCGGGCCCCACCAAGTCTCTGCC	723					
DB	303	GTCCCAAGTGTGGAAACCTCACACTCCCTCTGACTCCGGGCCCCACCAAGTCTCTGCC	362					
QY	724	AGCACAAAGGACCATGTACCAACACGGAGAGATCTTCAGTGGCCCATGAGCTGTCCCT	783					
DB	363	AGCACAAAGGACCATGTACCAACACGGAGAGATCTTCAGTGGCCCATGAGCTGTCCCT	422					
QY	784	CCGCTCTGCCCAACCAAGTGTCTCTGACGTGCAACAGAGGGCCAGATCTACTGGGGCC	843					
DB	423	CCGCTCTGCCCAACCAAGTGTCTCTGACGTGCAACAGAGGGCCAGATCTACTGGGGCC	482					
QY	844	TCACACCTGCCCGGAACCAAGTGTGCCAGACCCCTCCGCTTGCCAGACTCTCTGCTGCC	903					
DB	483	TCACACCTGCCCGGAACCAAGTGTGCCAGACCCCTCCGCTTGCCAGACTCTCTGCTGCC	542					
QY	904	AAGCTCTCAAGATGAGCAAGTGGCAATCGGATGAAGAGGACAGTGTGCAAGTCTCGTCC	963					
DB	543	AAGCTCTCAAGATGAGCAAGTGGCAATCGGATGAAGAGGACAGTGTGCAAGTCTCGTCC	602					
QY	964	ATGGGGTGAGACATCTCTCAGGATCCATGTTTCCAGTGTATCTCCAGTGTCTGGGAGAAAGAGAGGCCCGG	1023					

DB	603	ATGGGGTGAGACATCTCTCAGGATCCATGTTCCAGTGTCTGGGAGAAAGAGAGGCCCGG	662					
QY	1024	GCACCCAGCCCCCACTGCGCTCAGCGCCCTCTGAGCTTCTATCCCTCGCCACTTTCAGAC	1083					
DB	663	GCACCCAGCCCCCACTGCGCTCAGCGCCCTCTGAGCTTCTATCCCTCGCCACTTTCAGAC	722					
QY	1084	CAAAGGAGCAGGACGACCAACTGTCAGATCTCTCTGAGGAGAAACATAGAAGCCT	1143					
DB	723	CAAAGGAGCAGGACGACCAACTGTCAGATCTCTCTGAGGAGAAACATAGAAGCCT	782					
QY	1144	GTGTGCATGGCGGAGAGAGCTACTCCACGGGAGGTGTGGCACCCCGCCCTTCCGTGCT	1203					
DB	783	GTGTGCATGGCGGAGAGAGCTACTCCACGGGAGGTGTGGCACCCCGCCCTTCCGTGCT	842					
QY	1204	TCGGGCCCCCTTGGCTGCTATTCACCTGTGAGGATGGCCGACGACTGCCAGCGTG	1263					
DB	843	TCGGGCCCCCTTGGCTGCTATTCACCTGTGAGGATGGCCGACGACTGCCAGCGTG	902					
QY	1264	TGACCTGTCCCAACCGAGTACCCCTGCGTCAACCCGAGAAAGTGGCTGGGAGTCTGCA	1323					
DB	903	TGACCTGTCCCAACCGAGTACCCCTGCGTCAACCCGAGAAAGTGGCTGGGAGTCTGCA	962					
QY	1324	AGATTGCCCCAGAGCAAGACGACCTCGCCACAGTGTGAGATCAGTTCTTACAGGTGTC	1383					
DB	963	AGATTGCCCCAGAGCAAGACGACCTCGCCACAGTGTGAGATCAGTTCTTACAGGTGTC	1022					
QY	1384	CAAAGCAGCGGCGGCTCTCTCCACACATCGGTATCCCCAAGCCCGACACACCTGC	1443					
DB	1023	CAAAGCAGCGGCGGCTCTCTCCACACATCGGTATCCCCAAGCCCGACACACCTGC	1082					
QY	1444	GTGCTGTTGCTTGGAAACACGAGGCTTGGACTTTGGTGGAGATCTACTCTTGGAAAGTGG	1503					
DB	1083	GTGCTGTTGCTTGGAAACACGAGGCTTGGACTTTGGTGGAGATCTACTCTTGGAAAGTGG	1142					
QY	1504	TAAAGATGAGGAAACTGAGGCTCAGAGAGTGAAGTACCTGGCCCAAGGCCACACAGCC	1563					
DB	1143	TAAAG-----	1148					
QY	1564	AGATCTTCCACTTGAATCAAGAAAGTCAAGAAAGTCAAGAAAGTCTCCAGAAAGAGGCA	1623					
DB	1149	-GAATCTTCCACTTGAATCAAGAAAGTCAAGAAAGTCAAGAAAGTCTCCAGAAAGAGGCA	1207					
QY	1624	CAGCACTTCCGACTGCTGCTGGCCCGCCCAAGGCTCACTGGAAAGCTCTTCTAGCCAG	1683					
DB	1208	CAGCACTTCCGACTGCTGCTGGCCCGCCCAAGGCTCACTGGAAAGCTCTTCTAGCCAG	1267					
QY	1684	ACCTCGAGCTGAAGGTCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAGGCT	1743					
DB	1268	ACCTCGAGCTGAAGGTCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAGGCT	1327					
QY	1744	AACAGTTGAGATATGAGCTGTATAATTGTTTATATATATATATATATATATATATAT	1803					
DB	1328	AACAGTTGAGATATGAGCTGTATAATTGTTTATATATATATATATATATATATATAT	1387					
QY	1804	CATAACNTCAAAA	1817					
DB	1388	CATTACCCCTCAAAA	1401					

RESULT 32

AAD21152

ID AAD21152 standard; DNA; 1570 BP.

XX

AC AAD21152;

XX

DT 15-JAN-2002 (first entry)

XX Human chordin-like-2 (CHL-2) gene.

XX Human; chordin-like-2 protein; CHL-2; hypotensive; cardiac; cytostatic;

XX rheumatoid arthritis; cachexia; arrhythmia; osteoporosis; hepatitis;

XX hypertension; myocardial infarction; stomach cancer; ulcer; gene therapy;

antiinflammatory; tissue regeneration; osteoporosis; muscular dystrophy;
congestive heart failure; hepatoma; angina; ds.

Homo sapiens.

Key Location/Qualifiers
CDS 184..1473
/*tag= a
/product= "Human chordin-like-2 protein"
sig_peptide 184..243
/*tag= b
mat_peptide 244..1470
/*tag= c
/product= "Mature human chordin-like-2 protein"

WO200164885-A1.

07-SEP-2001.

02-MAR-2001; 2001WO-US06891.

02-MAR-2000; 2000US-186462P.

(AMGE-) AMGEN INC.

Zhang K, Linh C, Nakayama N;

WPI; 2001-648246/74.

P-PSDB; AAE12886, AAE12887.

Novel Chordin-like-2 polypeptides useful for diagnosing and treating
diseases and conditions affecting bone density, tissue regeneration,
skeletal muscle, heart, stomach and liver, and for wound healing -

Claim 1; Fig 3; 167pp; English.

The invention relates to chordin-like-2 (CHL-2) proteins and their
corresponding nucleic acid molecules. The invention also provides
pharmaceutical compositions and methods for the diagnosis, treatment,
amelioration, and/or prevention of diseases, disorders and conditions
associated with CHL2 proteins. Chordin-like-2 (CHL-2) proteins are useful
for diagnosing and treating diseases and conditions affecting bone
density (osteoporosis, osteoporosis, osteoarthritis and rheumatoid
arthritis), skeletal muscle (e.g., cachexia and muscular dystrophy),
heart (arrhythmia, angina, hypertension, myocardial infarction and
congestive heart failure), stomach (stomach cancer and ulcer), and
liver (hepatitis and hepatoma), for promoting tissue regeneration
and wound healing, for ex vivo expansion of haematopoietic stem cells
and gene therapy performed through such cells. CHL2 protein is also
useful for identifying CHL2 protein receptors. A selective binding
agent (SBA) or fragment is useful for detecting or quantitating the
amount of CHL2 protein. A transgenic non-human mammal is useful for
determining whether a compound inhibits CHL2 protein activity or
CHL2 protein production. The present DNA sequence is human
chordin-like-2 (CHL-2) gene.

Sequence 1570 BP; 340 A; 527 C; 400 G; 303 T; 0 other;

Query Match 67.3%; Score 1222.8; DB 22; Length 1570;
Best Local Similarity 93.8%; Pred. No. 0;
Matches 1307; Conservative 0; Mismatches 32; Indels 55; Gaps 1;
424 TTGGGCTGGAGCCTCTGGGACTAACATGGCACTGGTGGTGGCCAGCCAGACATCT 483
218 TGGACTCGGGCTGCTGTGGTTCCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 277
484 TCTGCTTTTCCATGGGAAGAGATACTCCCGGGGAGAGCTGGCACTCTACTTGGAGC 543
278 TCTGCTTTTCCATGGGAAGAGATACTCCCGGGGAGAGCTGGCACTCTACTTGGAGC 337
544 CACAAGCCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 603
338 CACAAGCCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 397

604 ACCGCTTCCACTGTCGGCTGTCCACTGCCGCCCGAGCTGTGACGGAGCCACAGCAATGCT 663
398 ACCGCTTCCACTGTCGGCTGTCCACTGCCGCCCGAGCTGTGACGGAGCCACAGCAATGCT 457
664 GTCCAAAGTGTGGAACTCCTCCTCTGAGCTCCGGGCCCCACCAAAAGTCTGCTGCC 723
458 GTCCAAAGTGTGGAACTCCTCCTCTGAGCTCCGGGCCCCACCAAAAGTCTGCTGCC 517
724 AGCAAAAGTGTGGAACTCCTCCTCTGAGCTCCGGGCCCCACCAAAAGTCTGCTGCC 783
518 AGCAAAAGTGTGGAACTCCTCCTCTGAGCTCCGGGCCCCACCAAAAGTCTGCTGCC 577
784 CCAGCTTCCCTGAGCACTCCTCCTCTGAGCTCCGGGCCCCACCAAAAGTCTGCTGCC 843
578 CCAGCTTCCCTGAGCACTCCTCCTCTGAGCTCCGGGCCCCACCAAAAGTCTGCTGCC 637
844 TCACAACTTCCCTGAGCACTCCTCCTCTGAGCTCCGGGCCCCACCAAAAGTCTGCTGCC 903
638 TCACAACTTCCCTGAGCACTCCTCCTCTGAGCTCCGGGCCCCACCAAAAGTCTGCTGCC 697
904 AGCTTCCCTGAGCACTCCTCCTCTGAGCTCCGGGCCCCACCAAAAGTCTGCTGCC 963
698 AGCTTCCCTGAGCACTCCTCCTCTGAGCTCCGGGCCCCACCAAAAGTCTGCTGCC 757
964 ATGGGCTGAGCACTCCTCCTCTGAGCTCCGGGCCCCACCAAAAGTCTGCTGCC 1023
758 ATGGGCTGAGCACTCCTCCTCTGAGCTCCGGGCCCCACCAAAAGTCTGCTGCC 817
1024 GCACCTTCCCTGAGCACTCCTCCTCTGAGCTCCGGGCCCCACCAAAAGTCTGCTGCC 1083
818 GCACCTTCCCTGAGCACTCCTCCTCTGAGCTCCGGGCCCCACCAAAAGTCTGCTGCC 877
1084 CCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1143
878 CCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 937
1144 GTGTGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1203
938 GTGTGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 997
1204 TCGGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1263
998 TCGGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1057
1264 TGACCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1323
1058 TGACCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1117
1324 AGATTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1383
1118 AGATTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1177
1384 CCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1443
1178 CCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1237
1444 GTGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1503
1238 GTGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1297
1504 TAAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1563
1298 TGAAG----- 1303
1564 AGATTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1623
1304 -GAATTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1362
1624 CAGCACTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1683
1363 CAGCACTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1422

1514 GGAAGTGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAAATCTTCC 1573
1213 GGAAGTGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAAAT-TTCC 1271
1574 ACTTGACTCAGATCAAGAACTCAGGAAGCAAGACTTCCAGAAAGGACACAGCACTTCC 1633
1272 ACTTGACTCAGATCAAGAACTCAGGAAGCAAGACTTCCAGAAAGGACACAGCACTTCC 1331
1634 GACTGCTCGCTGGCCCCCAGAAAGGTCACTGGAAGCTTCTTAGCCCCAGACCCTGGAGC 1693
1332 GACTGCTCGCTGGCCCCCAGAAAGGTCACTGGAAGCTTCTTAGCCCCAGACCCTGGAGC 1391
1694 TGAAGTCAAGCCGAGTCCAGACAAAGTGAACAAGACATAACAAGACCTAACAGTTGCA 1753
1392 TGAAGTCAAGCCGAGTCCAGACAAAGTGAACAAGACATAACAAGACCTAACAGTTGCA 1451
1754 GATATGAGCTGATAATGTGTTTATTATATTATTAATAAAGAGTTGCTAACACCATC 1813
1452 GATATGAGCTGATAATGTGTTTATTATATTATTAATAAAGAGTTGCTAACACCATC 1511
1814 AAAA 1817
1512 AAAA 1515
RESULT 36
BQ61159
D BQ61159 standard; cDNA; 1373 BP.
X C BQ61159;
X T 26-FEB-2003 (first entry)
X E Chordin-like homologue splice variant encoding sequence.
X W Neuroprotective; immunomodulator; cancer; chromosome 11;
W cytostatic; anti-inflammatory; gene therapy; nutritional supplement;
W wound; burn; ulcer; Alzheimer's disease; Huntington's disease;
W amyotrophic lateral sclerosis; autoimmune disorder; inflammation;
W vulnery; gene; ss.
X S Homo sapiens.
X N WO200231111-A2.
X N 18-APR-2002.
X D 11-OCT-2001; 2001WO-US27760.
X F 12-OCT-2000; 2000US-0687527.
X R (HYSE-) HYSEQ INC.
X I Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
I Xue AJ, Yang Y, Wehrman T, Drmanac RT;
R WPI; 2002-426278/45.
R N-PSDB; ABP43915.
X T New polypeptides and their encoded proteins, useful as nutritional
T sources or supplements, or in gene therapy, particularly for treating
T wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or
T inflammation -
S Claim 1; SEQ ID # 372; 357pp + sequence listing; English.
X C The invention relates to 446 newly isolated polynucleotide sequences.
X C The activity of polynucleotides of the invention may be described as,
C vulnery, neuroprotective, immunomodulator, cytostatic and
C anti-inflammatory. Compositions comprising nucleic acids of the invention
C are useful for treating a mammalian subject, or as nutritional sources or
C supplements. These are useful in gene therapy, particularly for treating

CC wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,
CC amyotrophic lateral sclerosis, autoimmune disorders, cancer or
CC inflammation. The nucleic acids and polypeptides are also useful in
CC diagnostic and research methods. The sequences given in records
CC ABQ60788-ABQ61233 represent polynucleotides of the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1373 BP; 308 A; 447 C; 363 G; 255 T; 0 other;
Query Match 57.1%; Score 1038.4; DB 24; Length 1373;
Best Local Similarity 99.9%; Pred. No. 1.4e-286;
Matches 1039; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 470 AGGCCACAGATGTTCTGCCCTTTTCCATGGGAAGAGATCTCCCGCGGAGAGCTGGCA 529
DB 187 ATGCCACAGATGTTCTGCCCTTTTCCATGGGAAGAGATCTCCCGCGGAGAGCTGGCA 246
QY 530 CCCTACTTGGAGCCACAAGCCCTGATCTACTGCTGGCTGTACTCTGTCTCAGAGGCGC 589
DB 247 CCCTACTTGGAGCCACAAGCCCTGATCTACTGCTGGCTGTACTCTGTCTCAGAGGCGC 306
QY 590 CATGTGAGTTGTTACCGCTTCCACTGTCGGCTGTCCACTGCCCGCCAGCCTGTGACGGA 649
DB 307 CCATGTGAGTTGTTACCGCTTCCACTGTCGGCTGTCCACTGCCCGCCAGCCTGTGACGGA 366
QY 650 GCCACAGCAATGCTGCCAAGTGTGGAACTTCACTCCCTCTGGACTCCGGGCCCC 709
DB 367 GCCACAGCAATGCTGCCAAGTGTGGAACTTCACTCCCTCTGGACTCCGGGCCCC 426
QY 710 ACCAAGTCTGCGCAGCACAAACGAGCCATGTACCAACAGGAGAGATCTTCACTGCCCCA 769
DB 427 ACCAAGTCTGCGCAGCACAAACGAGCCATGTACCAACAGGAGAGATCTTCACTGCCCCA 486
QY 770 TGAGCTGTTCCCTTCCCGCTTCCCAACAGCTGTGTCTCTGAGCTGCACAGAGGCGCA 829
DB 487 TGAGCTGTTCCCTTCCCGCTTCCCAACAGCTGTGTCTCTGAGCTGCACAGAGGCGCA 546
QY 830 GATCTACTGCGGCTCAACCTGCCCCGAAACAGGCTGCCAGCACCCCTTCCCGTGC 889
DB 547 GATCTACTGCGGCTCAACCTGCCCCGAAACAGGCTGCCAGCACCCCTTCCCGTGC 606
QY 890 AGACTCTGCTGCCAAGCTTCAAGATGAGGCAAGTGAAGTGAAGTGAAGAGACAG 949
DB 607 AGACTCTGCTGCCAAGCTTCAAGATGAGGCAAGTGAAGTGAAGAGACAG 666
QY 950 TGTGAGTCTGCTCCATGGGTTGAGACATCTCAGGATCCATGTTCCAGTGTCTGGAG 1009
DB 667 TGTGAGTCTGCTCCATGGGTTGAGACATCTCAGGATCCATGTTCCAGTGTCTGGAG 726
QY 1010 AAAGAGAGGCCCGGCGCACCCCGCTTCCAGCGCCCTCTGAGCTTCAATCCC 1069
DB 727 AAAGAGAGGCCCGGCGCACCCCGCTTCCAGCGCCCTCTGAGCTTCAATCCC 786
QY 1070 TCGCCACTTCAGACCCCAAGGAGCAGGAGCAGCAACTGTCAAGATGCTCTGAAGAGAA 1129
DB 787 TCGCCACTTCAGACCCCAAGGAGCAGGAGCAGCAACTGTCAAGATGCTCTGAAGAGAA 846
QY 1130 ACATAGAAGACCTGTGTGATGCGGGAAGACGTAATCTCCACGGGAGGTGGCACCC 1189
DB 847 ACATAGAAGACCTGTGTGATGCGGGAAGACGTAATCTCCACGGGAGGTGGCACCC 906
QY 1190 GGCTTCCGTCCTTCCGCGCCCTTCCGCTGATCTATGCACTGTGAGGATGGCGCCA 1249
DB 907 GGCTTCCGTCCTTCCGCGCCCTTCCGCTGATCTATGCACTGTGAGGATGGCGCCA 966
QY 1250 GGACTGCGAGCTGTGACCTGTCCACCGAGTACCCCTGCCGTACCCCGAGAAAGTGGC 1309
DB 967 GGACTGCGAGCTGTGACCTGTCCACCGAGTACCCCTGCCGTACCCCGAGAAAGTGGC 1026
QY 1310 TGGAGTGTGCAAGATTGCCCCAGAGGACAAAGCAGACCCCTGGCCACAGTGAATCAG 1369

Db 1027 TGGGAAGTGCTGCAAGATTGTCACAGAGGACAAAGCAGACCCCTGGCCACAGTGAGATCAG 1086

Qy 1370 TTCTACCAAGGTGTCACCAAGGACCGCGCGGTCCTCTCCACACATCGGTATCCCAAG 1429

Db 1087 TTCTACCAAGGTGTCACCAAGGACCGCGCGGTCCTCTCCACACATCGGTATCCCAAG 1146

Qy 1430 CCCAGACAACTGCGTGGCTTTGCTGGAACACAGAGGCTCGGACTTGTGTGGAGATCTA 1489

Db 1147 CCCAGACAACTGCGTGGCTTTGCTGGAACACAGAGGCTCGGACTTGTGTGGAGATCTA 1206

Qy 1490 CCTCTGGAAGCTGGTAAAG 1509

Db 1207 CCTCTGGAAGCTGGTAAAG 1226

RESULT 37

ABK12125

ID ABK12125 standard; cDNA; 1517 BP.

AC ABK12125;

XX 05-JUN-2002 (first entry)

XX Human cDNA encoding chordin homologue LP233.

XX Human; ss; gene; chordin homologue; LP233; neurological disorder;

KW Alzheimer's disease Parkinson's disease; wound; tissue repair;

KW bone fracture; spinal cord injury; pressure ulcer; diabetic ulcer;

KW venous stasis ulcer; burn; cardiovascular disorder; atherosclerosis;

KW thrombosis; heart failure; proliferative disorder; osteosarcoma;

KW breast cancer; leukaemia; prostate cancer; bone mineral density disorder;

KW osteopaenia-related disorder; fibrotic disorder; cirrhosis; Marfan's disease;

KW chronic asbestosis; restenosis; Gaucher's disease; Marfan's disease;

KW anaemia; diabetes mellitus; osteoporosis; transgenic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT misc_feature 234..720

FT /tag= a

FT /note= "This region is specifically claimed in claim 2"

FT CDS 235..723

FT /tag= b

FT /product= "LP233"

FT sig_peptide 235..315

FT /tag= c

FT misc_feature 315..720

FT /tag= d

FT /note= "This region is specifically claimed in claim 2"

FT mat_peptide 316..720

FT /tag= e

FT /label= Mature_LP233

XX WO200208277-A2.

PN 31-JAN-2002.

XX 05-JUL-2001; 2001WO-US16517.

XX 19-JUL-2000; 2000US-219359P.

PR 04-MAY-2001; 2001US-288892P.

XX (ELIL) LILLY & CO ELI.

XX Alvarez E, McEntire JK, Smith RC, Su EW;

PI WPI: 2002-280599/32.

DR P-PSDB; AAU78173.

XX Novel isolated LP polypeptide having significant sequence similarity to

PT cysteine-rich regions of chordin, useful for treating neurological,

PT cardiovascular, proliferative fibrotic and osteopaenia-related disorders

PT

XX Claim 3; Page 11-12; 149pp; English.

XX The invention relates to isolated LP polypeptides (which have

CC significant sequence similarity to the cysteine-rich regions of chordin

CC being LP226, LP233 and LP236) and encoding polynucleotides. The

CC mature portions of the LP proteins and the region of the nucleic acid

CC encoding them are also included. Also cell comprising the vector, an

CC anti-LP antibody and anti-agonists of the LP proteins. LP is useful in the

CC manufacture of a medicament. LP, LP polynucleotide Agonists or

CC antagonists of LP are useful for diagnosis and treatment of a

CC neurological disorder (e.g. Alzheimer's disease and

CC Parkinson's disease), a disorder requiring wound or tissue repair (where

CC the disorder is selected from bone fracture, spinal cord injury, pressure

CC ulcer, diabetic ulcer, venous stasis ulcer, and burn), a cardiovascular

CC disorder (e.g. atherosclerosis, thrombosis and heart failure), a

CC proliferative disorder such as osteosarcoma, breast cancer, leukaemia

CC and prostate cancer, a disorder associated with loss of bone mineral

CC density, an osteopaenia-related disorder, or a fibrotic disorder

CC (e.g. cirrhosis and chronic asbestosis) restenosis, Gaucher's disease,

CC Marfan's disease, anaemia, diabetes mellitus, osteoporosis and many other

CC diseases and disorders listed in the specification. LP is useful for

CC identifying compounds that bind to LP, and to isolate correlative

CC ligands. LP polynucleotide as hybridisation probes, in chromosome and

CC gene mapping, and in the generation of antisense RNA and DNA, for the

CC preparation of LP, for generating either transgenic or knock out animals,

CC and for chromosome identification. The antibody is useful in diagnostic

CC assays for LP, for affinity purification of LP and as diagnostic and

CC therapeutic agent. The present sequence encodes the LP protein LP233.

XX Sequence 1517 BP; 314 A; 510 C; 379 G; 314 T; 0 other;

SQ

Query Match 56.5%; Score 1026.4; DB 24; Length 1517;

Best Local Similarity 87.1%; Pred. No. 4.1e-283;

Matches 1214; Conservative 0; Mismatches 31; Indels 149; Gaps 2;

Qy 424 TTGGGCTGGAGCTCCTGGGACTTAACATGACATGCTGGTTCGGTTTGCAGGCGCCAGACATGT 483

Db 269 TGGGACTCGCGTGCTCTGTGTTCCCTCGACTCCACGCTCGAGCCGCCAGACATGT 328

Qy 484 TCTGCTTTTCCATGGGAGAGATATCTCCCGCGGAGAGCTGGCACCCCTACTTTGGAGC 543

Db 329 TCTGCTTTTCCATGGGAGAGATATCTCCCGCGGAGAGCTGGCACCCCTACTTTGGAGC 388

Qy 544 CACAAGCCTGATGTACTGCTGCGGTGTACTCTCAGAGGGCGCCATGTGAGTTGTT 603

Db 389 CACAAGCCTGATGTACTGCTGCGGTGTACTCTCAGAGGGCGCCATGTGAGTTGTT 448

Qy 604 ACGGCTCCACTGTCCGCTGTCCACTGCCCCCAGCCTGTGACGAGGCCACAGCAATGCT 663

Db 449 ACGGCTCCACTGTCCGCTGTCCACTGCCCCCAGCCTGTGACGAGGCCACAGCAATGCT 508

Qy 664 GTCCCAAGTGTGGAACTCCTCAGCTCCCTCTGAGCTCCGGGCCCCCAGCAAGTCTGTGCC 723

Db 509 GTCCCAAGTGTGGAACTCCTCAGCTCCCTCTGAGCTCCGGGCCCCCAGCAAGTCTGTGCC 568

Qy 724 AGCACAAACGGGACCATGTACACACACGAGAGATCTTCAGTGCCCATGAGTGTTCCTT 783

Db 569 AGCACAAACGGGACCATGTACACACACGAGAGATCTTCAGTGCCCATGAGTGTTCCTT 628

Qy 784 CCGGCTGCCCCAACCAAGTGTGCTCTGAGCTGCACAGAGGGCCAGATCTACTGGGGCC 843

Db 629 CCGGCTGCCCCAACCAAGTGTGCTCTGAGCTGCACAGAGGGCCAGATCTACTGGGGCC 666

Qy 844 TCACACCTGCCCGGAACAGGCTGCCAGCACCCCTCCCGTGCAGAGATCTCTGTGTGCC 903

Db 667 ----- 666

Qy 904 AAGCTGCAAGATGAGGCAAGTGTGAGCAATCGATGAAGAGGACAGTGTGAGTCTGCTCC 963

Db 667 -----ATGAGGCAAGTGTGAGCAATCGATGAAGAGGACAGTGTGAGTCTGCTCC 714

964 ATGGGTGAGACATCTCCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGAGCCCGG 1023
715 ATGGGTGAGACATCTCCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGAGCCCGG 774
1024 GCACCCAGCCCGACCTGAGCGGCTCAGCGGCTCTGAGCTTCACTCCCTGCCACTTCAGAC 1083
775 GCACCCAGCCCGACCTGAGCGGCTCAGCGGCTCTGAGCTTCACTCCCTGCCACTTCAGAC 834
1084 CCAAGGAG 1143
835 CCAAGGAG 894
1144 GTGTGATGCGGAG 1203
895 GTGTGATGCGGAG 954
1204 TCGGCCCCCTTGCCTGATCTCCTGATCTCCTGATCTCCTGATCTCCTGATCTCCTGATCT 1263
955 TCGGCCCCCTTGCCTGATCTCCTGATCTCCTGATCTCCTGATCTCCTGATCTCCTGATCT 1014
1264 TGACCTGTGCGGAG 1323
1015 TGACCTGTGCGGAG 1074
1324 AGATTTGCCAG 1383
1075 AGATTTGCCAG 1134
1384 CCAAGGAG 1443
1135 CCAAGGAG 1194
1444 GTGCTTTGCGGAG 1503
1195 GTGCTTTGCGGAG 1254
1504 TAAAGATGAG 1563
1255 TAAAG----- 1260
1564 AGATTTGCCAG 1623
1261 -GAATTTGCCAG 1319
1624 CAGCACTTCGAGTCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1683
1320 CAGCACTTCGAGTCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1379
1684 ACCCTGGAGTGAAGGTCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1743
1380 ACCCTGGAGTGAAGGTCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1439
1744 AACAGTTGCGAGATGAGCTGATATTTGTTTATTATATATATATATATATATATATATAT 1803
1440 AACAGTTGCGAGATGAGCTGATATTTGTTTATTATATATATATATATATATATATATAT 1499
1804 CATAACCATCAAAA 1817
1500 CATTACCTCAAAA 1513

Query Match 41.3%; Score 750; DB 22; Length 1839;
Best Local Similarity 75.5%; Pred. No. 6.5e-204;
Matches 1004; Conservative 0; Mismatches 255; Indels 71; Gaps 3;
QY 472 GCCCAGACATGTTCTGCTTTTCCATGGGAGAGATATCTCCCGCGGAGAGTGGCACC 531
Db 553 GCTCGGCAAGTCTGCTTTTCCGTTGAAAGATATATACCCCGGAGAGTGGCACC 612
QY 532 CCTACTTGGAGCCACAGGCTGATGTTACTGCTCGCTGTTACTGCTCAGAGGGGCCCC 591
Db 613 CCTACTTGGAGCCACAGGCTGATGTTACTGCTCGCTGTTACTGCTCAGAGTGGAC 672
QY 592 ATGTGAGTTTACCGCTCCACTGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 651

hypertension; myocardial infarction; stomach cancer; ulcer; gene therapy;
antiinflammatory; tissue regeneration; osteoporosis; muscular dystrophy;
congestive heart failure; hepatoma; angina; chromosome 7; ds.
Mus musculus.
Key Location/Qualifiers
CDS 471..1751
/*tag= a
/product= "Murine chordin-like-2 protein"
sig_peptide 471..530
/*tag= b
mat_peptide 531..1748
/*tag= c
/product= "Mature murine chordin-like-2 protein"
WO200164885-A1.
07-SEP-2001.
02-MAR-2001; 2001WO-US06891.
02-MAR-2000; 2000US-186462P.
(AMGE-) AMGEN INC.
Zhang K, Linh C, Nakayama N;
WPI: 2001-648246/74.
P-PSDB; AAE12884, AAE12885.
Novel Chordin-like-2 polypeptides useful for diagnosing and treating
diseases and conditions affecting bone density, tissue regeneration,
skeletal muscle, heart, stomach and liver, and for wound healing -
Claim 1; Fig 1; 167pp; English.
The invention relates to chordin-like-2 (CHL-2) proteins and their
corresponding nucleic acid molecules. The invention also provides
pharmaceutical compositions and methods for the diagnosis, treatment,
amelioration, and/or prevention of diseases, disorders and conditions
associated with CHL2 proteins. Chordin-like-2 (CHL-2) proteins are useful
for diagnosing and treating diseases and conditions affecting bone
density (osteoporosis, osteoporosis, osteoarthritis and rheumatoid
arthritis), skeletal muscle (e.g., cachexia and muscular dystrophy),
heart (arrhythmia, angina, hypertension, myocardial infarction and
congestive heart failure), stomach (stomach cancer and ulcer), and
liver (hepatitis and hepatoma), for promoting tissue regeneration
and wound healing, for ex vivo expansion of haematopoietic stem cells
and gene therapy performed through such cells. CHL2 protein is also
useful for identifying CHL2 protein receptors. A selective binding
agent (SBA) or fragment is useful for detecting or quantitating the
amount of CHL2 protein. A transgenic non-human mammal is useful for
determining whether a compound inhibits CHL2 protein activity or
CHL2 protein production. The present DNA sequence is murine
chordin-like-2 (CHL-2) gene located on chromosome 7.

Sequence 1839 BP; 394 A; 618 C; 413 G; 414 T; 0 other;
Query Match 41.3%; Score 750; DB 22; Length 1839;
Best Local Similarity 75.5%; Pred. No. 6.5e-204;
Matches 1004; Conservative 0; Mismatches 255; Indels 71; Gaps 3;
QY 472 GCCCAGACATGTTCTGCTTTTCCATGGGAGAGATATCTCCCGCGGAGAGTGGCACC 531
Db 553 GCTCGGCAAGTCTGCTTTTCCGTTGAAAGATATATACCCCGGAGAGTGGCACC 612
QY 532 CCTACTTGGAGCCACAGGCTGATGTTACTGCTCGCTGTTACTGCTCAGAGGGGCCCC 591
Db 613 CCTACTTGGAGCCACAGGCTGATGTTACTGCTCGCTGTTACTGCTCAGAGTGGAC 672
QY 592 ATGTGAGTTTACCGCTCCACTGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 651

ESULT 38
AD211151
D AAD211151 standard; DNA; 1839 BP.
C AAD211151;
X
T 15-JAN-2002 (first entry)
E Murine chordin-like-2 (CHL-2) gene.
X Murine; chordin-like-2 protein; CHL-2; hypotensive; cardiast; cytostatic;
X Rheumatoid arthritis; cachexia; arrhythmia; osteoporosis; hepatitis;
W

673 ATGTGAATTGTTACGGCTCGCTGCCACCCCTTCACTGCTCACAGCCTGTGATGAGC 732
652 CACAGCAATGCTGTCCTCCAGTGTGTGGACCTCACACTCCCTCTGACCTCCGGGCCAC 711
733 CACAGCAATGCTGTCCTCCAGTGTGTGGACCTCACACTCCCTCTGACCTCCGGGCCAC 792
712 CAAAGTCTCTGCGCAGCACACGGGACCATGTAGCAACACGAGAGATCTTCAGTGCCTCATG 771
793 TAAAGTCTCTGCGCAGCTCAATGAGACCATATCAACATGAGAGATCTTCAGTGCCTCATG 852
772 AGCTGTTCCCTCTCCGCTGCCCCACCACTGCTCTGACAGCTGACAGAGGCCAG 831
853 AGCTGTTCCCTCTCCGCTGCCCCACCACTGCTCTGACAGCTGACAGAGGCCAG 912
832 TCTACTGCGGCTCACAACTGCGCCGACCAAGGCTGCCAGCACCCCTCCGCTGCCAG 891
913 CTTACTGTGGTCTCATGACCTGCTCTGAAACCCAGCTGCCACCACTCCCTCTGCTG 972
892 ACTCTGCTGCCAAGCTCTCAAGATGAGCAAGTGAAGCAATCGGATGAAGAGACAGTG 951
973 ATTCTGCTGTGACACCTCTCAAGACAGACAACTGAGAGTTCACAGAGAAACTTGA 1032
952 TGCAGTCTGCTCCATGGGTGAGACATCTCTCAGGATCCATGTTCCAGTGTGCTGGAGAA 1011
1033 CACAGCTGAGCATGGAGAGACATTCACAGGATCCATGCTC-----GGAGA 1080
1012 AGAGAGCCCGGCGACCCAGCCCTCTGCTGCTGAGGCTCTGAGCTTCTGCTCTCCTC 1071
1081 GGAGAGGCCCGGCGACCCAGCCCTCTGCTGCTGAGGCTCTGAGCTTCTGCTCTCCTC 1140
1072 GCCACTTCAGACCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1131
1141 GCCACTTCAGTCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
1132 ATAAGAAAGCTGTGTGCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1191
1201 ATAAAGAGCTGTGACACACACAACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260
1192 CTTCCGCTGCTTGGCGCCCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1251
1261 CTGTGCTCTCTTGGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
1252 ACTGCGAGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1311
1321 ACTGCGAGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
1312 GGAAGTCTGCAAGATTTGCCAGAGACAAAGCAGACCTTCCGACAGTGCAGATCAGTT 1371
1381 GGAAGTCTGCAAGATTTGCCAGAGACAAAGCAGACCTTCCGACAGTGCAGATCAGTT 1440
1372 CTACCAAGTGTCCCAAGGACCCGGGCGGGTCTCTGCTCCACACATCGGTATCCCAAGCC 1431
1441 CCACCCGCTGCTCCAGGTAACAGGCTACAGGCTTCCAGGCTGACAGTTCGCACTCCAGCC 1500
1432 CAGACAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1491
1501 CAGACAGCCTACACCGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
1492 TCTGGAAGCTGTTAAAGATGAGGAAACTGAGGCTCAGAGGCTGAGTACTTGGCCCA 1551
1561 TTTGGAAGCTGTTGGAAG----- 1578
1552 GGCCACACAGCCGAATCTTCCACTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1611
1579 -----GAACTCTACCTTGGTTTCAAGTCAAGAGAGTCAAGAGGCAAGATTTC 1625
1612 CAGAAAGAGGACAGCACTTCCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1671
1626 CAGAAAGAGGCTCAGAACTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1685
1672 TTCTAGCCCAAGCCCTGGAGCTGAAGCTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1731
1686 TTCTAGCCCAAGCTCAGAGAGCTGAAAGTTACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1745

Qy 1732 TAACAAAGA-----CCTAACAGTTGCAGATATGAGCTGTATAATTTGTTATTATATT 1787
Db 1746 TTATAGCAAGGACCTAAAGAGTTGCAGATACGAGTTTATTTGTTATTATATT 1805
Qy 1788 AATAAATAAG 1797
Db 1806 AATAAAGAAG 1815

RESULT 39

AAZ41343/c

ID AAZ41343 standard; cDNA; 807 BP.

XX AAZ41343;

DT 19-JAN-2000 (first entry)

DE Human normal uterus tissue derived cDNA 19.

XX Human; uterus; cancer; treatment; anticancer; cytostatic; gene therapy;

KW EST; expressed sequence tag; ss.

XX Homo sapiens.

XX DE19817946-A1.

XX 21-OCT-1999.

XX 17-APR-1998; 98DE-1017946.

XX 17-APR-1998; 98DE-1017946.

XX (META-) METAGEN GES GENOMFORSCHUNG MBH.

XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;

XX WPI: 1999-591956/51.

XX P-PSDB; AAY69887, AAY69888, AAY69889.

XX New nucleic acid sequences expressed in normal uterine tissues, and
PT derived polypeptides, for treatment of uterine cancer and
PT identification of therapeutic agents

XX Claim 3; Page 86; 154pp; German.

XX This invention describes novel cDNA sequences (A) highly expressed in
normal uterine tissue which can have anticancer and cytostatic activity
and can be used for gene therapy. (A) are used (i) for recombinant
expression of polypeptides (B) and (ii) to isolate complete genes.
XX (B) are used (i) to identify agents suitable for treatment of uterine
cancer; (ii) directly for treating this form of cancer (including of
expression from gene therapy vectors) and (iii) for generation of
specific antibodies. (A) are identified by assembling ESTs (expressed
sequence tags) from a particular tissue type before comparison of the
expression patterns. This allows a significantly longer fragment of the
gene to be revealed, so should reduce the number of failures associated
with the fact that ESTs from different libraries may represent
different parts of the same unknown gene, distorting the estimated
frequency of occurrence in a particular tissue. AAZ41325-241385
XX represent the human uterine tissue derived cDNA fragments of the
XX invention which encode the protein fragments represented in
XX AAY59838-Y59892.

SQ Sequence 807 BP; 149 A; 203 C; 252 G; 203 T; 0 other;

Query Match 37.2%; Score 675.4; DB 20; Length 807;

Best Local Similarity 91.3%; Pred. No. 9.6e-183;

Matches 784; Conservative 0; Mismatches 16; Indels 59; Gaps 4;

Qy 962 CCATGGGGTGCAGACATCTCTCAGGATCCATGTT-CCAGTGCATCTGGGAGAAAGAGGCC 1020

Db 804 CCACCGCTTAGACACCCCTCAGCATCTCTTCCCATCCATCTCTGGAGAGAGGCC 745

2Y 1021 CCGGC-ACCCAGCCCCCACTGGCTCAGCGCCCTCTGAGCTTCATCCCTCGCATTTC 1079
2b 744 CGGTGACCCAGCCCCCACTGGCTCAGCGCCCTCTGAGCTTCATCCCTCGCATTTC 685
2Y 1080 AGACCCAGGAGCAGGAGCAGCAAACTGTCAAGATCGTCTGAAGAGAGAAACATAGAAA 1139
2b 684 AGACCCAGGAGCAGGAGCAGCAAACTGTCAAGATCGTCTGAAGAGAGAAACATAGAAA 625
2Y 1140 GCCTGTGTGATGGCGGGAAGACGTACTCCACGGGAGGTGTGGCACCCGGCTTCCTCGT 1199
2b 624 GCCTGTGTGATGGCGGGAAGACGTACTCCACGGGAGGTGTGGCACCCGGCTTCCTCGT 565
2Y 1200 GCCTTGGCCCTTGGCCCTGATCTATGCACTGTGAGATGGCGCCAGGACTGCCAG 1259
2b 564 GCCTTGGCCCTTGGCCCTGATCTATGCACTGTGAGATGGCGCCAGGACTGCCAG 505
2Y 1260 CCGTGTGACCTTCCACAGAGTACCCCTGCTCACCAGAGAACTGCTGGAGATGC 1319
2b 504 CCGTGTGACCTTCCACAGAGTACCCCTGCTCACCAGAGAACTGCTGGAGATGC 445
2Y 1320 TGCAAGATTTCCACAGAGCAAAAGCAGACCTCGGCCACAGTGAGATCAGTTCTACCAAG 1379
2b 444 TGCAGATTTGCCACAGAGCAAAAGCAGACCTCGGCCACAGTGAGATCAGTTCTACCAAG 385
2Y 1380 TGTCCCAAGCAGCGGCGGGTCTCTGTCCACATCGGTATCCCAAA--GCCAGACA 1437
2b 384 TGTCCCAAGCAGCGGCGGGTCTCTGTCCACATCGGTATCCCAAAAGGCCAGACA 325
2Y 1438 ACTGCGTGGTTTGGCCCTGGAACAGAGGCTCGGACTTGTGGAGATCTACTCTGGA 1497
2b 324 ACTGCGTGGTTTGGCCCTGGAACAGAGGCTCGGACTTGTGGAGATCTACTCTGGA 265
2Y 1498 AGCTGGTAAAGATGAGAAACTGAGGCTCAGAGGTGAAGTACTCGGCCCAAGGCCAC 1557
2b 264 AGCTGGTAAAG----- 253
2Y 1558 ACAGCCAGATCTTCCACTTGACTCAGATCAAGAAAGTCAGGAGCAAGACTTCCAGAA 1617
2b 252 -----GAATCTTCCACTTGACTCAGATCAAGAAAGTCAGGAGCAAGACTTCCAGAA 200
2Y 1618 GAGGCACAGCACTTCCGACTGCTCGTGGCCGCCACGAGGTCACTGGAACTGCTTCTTA 1677
2b 199 GAGGCACAGCACTTCCGACTGCTCGTGGCCGCCACGAGGTCACTGGAACTGCTTCTTA 140
2Y 1678 GCCCAGACCTGGAGCTGAAGTCAAGGCTCAGGCTCAGACAAAGTGACCAAGACATAACAA 1737
2b 139 GCCCAGACCTGGAGCTGAAGTCAAGGCTCAGGCTCAGACAAAGTGACCAAGACATAACAA 80
2Y 1738 AGACCTAACAGTTGCAGATATGAGCTGTATATTTGTTATATATATATATATATATAG 1797
2b 79 AGACCTAACAGTTGCAGATATGAGCTGTATATTTGTTATATATATATATATATATAG 20
2Y 1798 AAGTTGCATAACCATCAA 1816
2b 19 AAGTTGCATAACCTCAAA 1

RESULT 40
AAS75270/C
D AAS75270 standard; cDNA; 622 BP.
X
X AAS75270;
X
X 13-FEB-2002 (first entry)
X
X DNA encoding novel human diagnostic protein #11074.
X
X Human; chromosome mapping; gene mapping; gene therapy; forensic;
X food supplement; medical imaging; diagnostic; genetic disorder; ss.
X
X Homo sapiens.
X

PN WO200175067-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US08631.
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX P-PSDB; ABG11083.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity
XX
XX Claim 1; SEQ ID No 11074; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAS64197-AAS94564 represent novel human
XX diagnostic coding sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 622 BP; 115 A; 155 C; 170 G; 182 T; 0 other;
XX
XX Query Match 29.9%; Score 543.6; DB 23; Length 622;
XX Best Local Similarity 97.7%; Pred. No. 4.6e-145;
XX Matches 594; Conservative 0; Mismatches 9; Indels 5; Gaps 4;
QY 1215 CCCTGTCATCTTATGCACCTGTGAGGATGCGCCGAGGACTGCCAGCGTGTGACCTGTCCC 1274
Db 622 CCATGCATCTTATGCACCTGTGAGGATGCGCCGAGGACTGCCAGCGTGTGACCTGTCCC 563
QY 1275 ACCGAGTACCCCTGCGTCAACCCGAGAAAGTGGTGGAAAGTGTGCAAGATTGCCCCA 1334
Db 562 ACGAAGTACCCCTGCGGTCAACCTGAGATAGTGGTGGAAAGTGTGCAAGATTGCCCCA 503
QY 1335 GAGGACAAAGCAGACCCCTGGCCACAGTGAATCTTACAGGTTGTCACCAAGGACCG 1394
Db 502 GAGGACAAAGCAGACCCCTGGCCACAGTGAATCTTACAGGTTGTCACCAAGGACCG 443
QY 1395 GGCCGGTCTCTGTCACACATCGGTATCCCAAGCCAGACAACTGCGTCTGCTTTGCC 1454
Db 442 GGCCGGTCTCTGTCACACATCGGTATCCCAAGCCAGACAACTGCGTCTGCTTTGCC 383
QY 1455 C--TGGAACACGAGGCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGTTAAAGATG 1512
Db 382 CTTGGAAACACGAGGCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGTTAAAGATG 323
QY 1513 AGGAAC--TGAGGCTCA--GAGAGGTGAAGTACTCTGCGCCCAAGGCCACAGCAGGAATCT 1570

Search completed: January 31, 2004, 01:00:37
Job time : 516 secs

RESULT 2

1	PRIOR FILING DATE: 1998-09-23	
2	PRIOR APPLICATION NUMBER: 60/101476	
3	PRIOR FILING DATE: 1998-09-23	
4	PRIOR APPLICATION NUMBER: 60/101477	
5	PRIOR FILING DATE: 1998-09-23	
6	PRIOR APPLICATION NUMBER: 60/101479	
7	PRIOR FILING DATE: 1998-09-23	
8	PRIOR APPLICATION NUMBER: 60/101738	
9	PRIOR FILING DATE: 1998-09-24	
10	PRIOR APPLICATION NUMBER: 60/101741	
11	PRIOR FILING DATE: 1998-09-24	
12	PRIOR APPLICATION NUMBER: 60/101743	
13	PRIOR FILING DATE: 1998-09-24	
14	PRIOR APPLICATION NUMBER: 60/101915	
15	PRIOR FILING DATE: 1998-09-24	
16	PRIOR APPLICATION NUMBER: 60/101916	
17	PRIOR FILING DATE: 1998-09-24	
18	PRIOR APPLICATION NUMBER: 60/102207	
19	PRIOR FILING DATE: 1998-09-29	
20	PRIOR APPLICATION NUMBER: 60/102240	
21	PRIOR FILING DATE: 1998-09-29	
22	PRIOR APPLICATION NUMBER: 60/102307	
23	PRIOR FILING DATE: 1998-09-29	
24	PRIOR APPLICATION NUMBER: 60/102330	
25	PRIOR FILING DATE: 1998-09-29	
26	PRIOR APPLICATION NUMBER: 60/102331	
27	PRIOR FILING DATE: 1998-09-29	
28	PRIOR APPLICATION NUMBER: 60/102484	
29	PRIOR FILING DATE: 1998-09-30	
30	PRIOR APPLICATION NUMBER: 60/102487	
31	PRIOR FILING DATE: 1998-09-30	
32	PRIOR APPLICATION NUMBER: 60/102570	
33	PRIOR FILING DATE: 1998-09-30	
34	PRIOR APPLICATION NUMBER: 60/102571	
35	PRIOR FILING DATE: 1998-09-30	
36	PRIOR APPLICATION NUMBER: 60/102684	
37	PRIOR FILING DATE: 1998-10-01	
38	PRIOR APPLICATION NUMBER: 60/102687	
39	PRIOR FILING DATE: 1998-10-01	
40	PRIOR APPLICATION NUMBER: 60/102965	
41	PRIOR FILING DATE: 1998-10-02	
42	PRIOR APPLICATION NUMBER: 60/103258	
43	PRIOR FILING DATE: 1998-10-06	
44	PRIOR APPLICATION NUMBER: 60/103314	
45	PRIOR FILING DATE: 1998-10-07	
46	PRIOR APPLICATION NUMBER: 60/103315	
47	PRIOR FILING DATE: 1998-10-07	
48	PRIOR APPLICATION NUMBER: 60/103328	
49	PRIOR FILING DATE: 1998-10-07	
50	PRIOR APPLICATION NUMBER: 60/103395	
51	PRIOR FILING DATE: 1998-10-07	
52	PRIOR APPLICATION NUMBER: 60/103396	
53	PRIOR FILING DATE: 1998-10-07	
54	PRIOR APPLICATION NUMBER: 60/103401	
55	PRIOR FILING DATE: 1998-10-07	
56	PRIOR APPLICATION NUMBER: 60/103449	
57	PRIOR FILING DATE: 1998-10-06	
58	PRIOR APPLICATION NUMBER: 60/103633	
59	PRIOR FILING DATE: 1998-10-08	
60	PRIOR APPLICATION NUMBER: 60/103678	
61	PRIOR FILING DATE: 1998-10-08	
62	PRIOR APPLICATION NUMBER: 60/103679	
63	PRIOR FILING DATE: 1998-10-08	
64	PRIOR APPLICATION NUMBER: 60/103711	
65	PRIOR FILING DATE: 1998-10-08	
66	PRIOR APPLICATION NUMBER: 60/104257	
67	PRIOR FILING DATE: 1998-10-14	
68	PRIOR APPLICATION NUMBER: 60/104987	
69	PRIOR FILING DATE: 1998-10-20	
70	PRIOR APPLICATION NUMBER: 60/105000	
71	PRIOR FILING DATE: 1998-10-20	
72	PRIOR APPLICATION NUMBER: 60/105002	
73	PRIOR FILING DATE: 1998-10-20	

Dd	1341	GTCGCTTTGGCCCTCGAACAACAGAGGCCTCGAGCTTGTGGAGATCTACTCCTCGGAAGCTGG	1400
Qy	1504	TAAAAAGATGAGAAACTGAGGCTTCAGAGAGTGTAAGTACCTGGCCCCCAAGGCCACACAGCC	1563
Dd	1401	TAAAAGATGAGAAACTGAGGCTTCAGAGAGTGTAAGTACCTGGCCCCCAAGGCCACACAGCC	1460
Qy	1564	AGAATCTTCCACTTGTACTCAGATCAAGAAGTCCAGGAAGCAAGACTTCCAGAAAGAGGCA	1623
Dd	1461	AGAATCTTCCACTTGTACTCAGATCAAGAAGTCCAGGAAGCAAGACTTCCAGAAAGAGGCA	1520
Qy	1624	CAGCATCTCCGACTGCTCGCTGGCCCCCACGAAGGTCACCTGGGAACGCTTCTTCTAGCCCAG	1683
Dd	1521	CAGCATCTCCGACTGCTCGCTGGCCCCCACGAAGGTCACCTGGGAACGCTTCTTCTAGCCCAG	1580
Qy	1684	ACCCTGGAGCTGAAGGTCAGGCCACCTCCAGACAAAGTGACCAAGACATACCAAGACCT	1743
Dd	1581	ACCCTGGAGCTGAAGGTCAGGCCACCTCCAGACAAAGTGACCAAGACATACCAAGACCT	1640
Qy	1744	AACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATATTTAATAAATAAGAGTTG	1800
Dd	1641	AACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATATTTAATAAATAAGAGTTG	1700
Qy	1804	CATAACCATCAAAA	1817
Dd	1701	CATTACCTCAAAA	1714

RESULT 4
US-10-012-231A-141
; Sequence 141, Application US/10012231A
; Publication No. US20040014130A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C23
; CURRENT APPLICATION NUMBER: US/10/012,231A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 141
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-231A-141

Query March		73.9%;	Score 1342.8;	DB 12;	Length 1732;
Best Local Similarity		97.7%;	Pred. No. 0;	Mismatches	32; Indels 0; Gaps 0;
Matches 1362;		Conservative			

Qy	424	TTGGCTCGAGGCTCCTGGGACTAACATGGCACTGGTTCGGTTTTGGCCAGGCCCCACACATGT	483
Dd	321	TGGNACTCGGCTGCTCTGTGTTCCCTCGACTCCACGCTCGAGCCGCCAGACATGT	380
Qy	484	TCTGCTTTTCCATGGGAAGAGATACCTCCCGGGGAGAGCTGGCACCCCTACTTTGGAGC	543
Dd	381	TCTGCTTTTCCATGGGAAGAGATACCTCCCGGGGAGAGCTGGCACCCCTACTTTGGAGC	440
Qy	544	CACAAGGCTGATGACTGCTCGCTGATCTGCTCAGAGGGCGGCCATGTGAGTTGTT	603

921	GC	ACCCAGC	CCCCACTGG	CCCTCAG	CGCCCTCTG	AGCTTCA	TCCTCG	CACCTC	CAGAC	980		
1084	CC	AGGAGC	AGGAGCA	CAACTGT	CAAGATCT	CTG	AAGGAG	AAACAT	AAGAA	GCGT 1143		
981	CC	AGGAGC	AGGAGCA	CAACTGT	CAAGATCT	CTG	AAGGAG	AAACAT	AAGAA	GCGT 1040		
1144	GT	GTGCAT	TGGGGG	GAAGACT	ACTAC	CCACGG	GAGGTGTG	GCACCG	CGCTTC	CGTGCCT 1203		
1041	GT	GTGCAT	TGGGGG	GAAGACT	ACTAC	CCACGG	GAGGTGTG	GCACCG	CGCTTC	CGTGCCT 1100		
1204	TC	GGCCCT	TG	CCCTGC	ATCTCT	ATG	CACCTGT	GAGGATG	CGCCG	CAGGACTGC 1263		
1101	TC	GGCCCT	TG	CCCTGC	ATCTCT	ATG	CACCTGT	GAGGATG	CGCCG	CAGGACTGC 1166		
1264	TG	ACTGT	CCAC	CAGGTAC	CCCTCG	CTC	ACCCG	AGAAGT	CGCTGG	GAAGTCTGCA 1323		
1161	TG	ACTGT	CCAC	CAGGTAC	CCCTCG	CTC	ACCCG	AGAAGT	CGCTGG	GAAGTCTGCA 1220		
1324	AG	ATTG	CC	CAGAGCA	AAAGCAG	ACCTGG	CCACAGT	GAGATC	GAGTTCT	TACCAAGTGTG 1383		
1221	AG	ATTG	CC	CAGAGCA	AAAGCAG	ACCTGG	CCACAGT	GAGATC	GAGTTCT	TACCAAGTGTG 1280		
1384	CC	AAGGC	ACCG	GGCGGGT	CTCGT	CCAC	ATCGGTAT	TCCC	AAAGCC	CACAACTGTC 1443		
1281	CC	AAGGC	ACCG	GGCGGGT	CTCGT	CCAC	ATCGGTAT	TCCC	AAAGCC	CACAACTGTC 1340		
1444	GT	CGTTTT	GC	CCCTG	GNACAG	GAGGCT	CG	ACTTGGT	TGGAGATCT	ACCTCTTGG	AAAGTCTG 1503	
1341	GT	CGTTTT	GC	CCCTG	GNACAG	GAGGCT	CG	ACTTGGT	TGGAGATCT	ACCTCTTGG	AAAGTCTG 1400	
1504	TA	AAAGAT	GAG	AAACTG	AGGCTC	AG	AGAGGT	GAAGTAC	CTGG	CCCAAGGCC	CACACAGCC 1563	
1401	TA	AAAGAT	GAG	AAACTG	AGGCTC	AG	AGAGGT	GAAGTAC	CTGG	CCCAAGGCC	CACACAGCC 1460	
1564	AG	AATCTT	CC	ACTTGA	CTCAG	ATCA	AGAAAGT	CAGGAAG	CAAGACTT	CCAGAA	GAGGCA 1623	
1461	AG	AATCTT	CC	ACTTGA	CTCAG	ATCA	AGAAAGT	CAGGAAG	CAAGACTT	CCAGAA	GAGGCA 1520	
1624	C	AGCACTT	CC	GACTGT	CGTGG	CCCC	CC	CGAAGT	C	ACTGGA	AGCTCTTCTAG	CCCCAG 1683
1521	C	AGCACTT	CC	GACTGT	CGTGG	CCCC	CC	CGAAGT	C	ACTGGA	AGCTCTTCTAG	CCCCAG 1580
1684	ACC	TGG	AGCTGA	AGGTCA	CGG	CCAGTCC	AG	CAAAAGT	GAC	CAAG	CATATA	CAAGACCT 1743
1581	ACC	TGG	AGCTGA	AGGTCA	CGG	CCAGTCC	AG	CAAAAGT	GAC	CAAG	CATATA	CAAGACCT 1640
1744	AA	CAGTTG	CAGATAT	GAGCTGT	ATAA	TGTTG	TTATTA	TATATTA	TATTA	TAATAA	TAAAGAGTTG 1803	
1641	AA	CAGTTG	CAGATAT	GAGCTGT	ATAA	TGTTG	TTATTA	TATATTA	TATTA	TAATAA	TAAAGAGTTG 1700	
1804	CA	TAACCAT	CAAAA	1817								
1701	CA	TTACCTT	CAAAA	1714								

RESULT 7
US-10-006-130A-141
; Sequence 141, Application US/10006130A
; Publication No. US20030148375A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.

```

; APPLICANT: Pan, James
; APPLICANT: Pioni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C7
; CURRENT APPLICATION NUMBER: US/10/006,130A
; CURRENT FILING DATE: 2002-03-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 141
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-006-130A-141

Query Match      73.9%;      Score 1342.8;  DB 13;  Length 1732;
Best Local Similarity 97.7%;  Pred. No. 0;
Matches 1362;  Conservative 0;  Mismatches 32;  Indels 0;  Gaps 0;

QY  424  TTGGGCTGGAGCCTCTCTGGACTAAATGGCACTGGTCTGGTGTTCAGGCCAGGCCAGACATGTT 483
DB    321  TGGGACTCGCGCTGCTCTGGTTTCCCCCTGGACTCCACGCTCGAGCGCCGCCAGACATGTT 380
QY  484  TCTGCCCTTTCCATGGGAGAGATACTCCCGGCGAGAGCTGSCACCCCTACTTGGAGC 543
DB    381  TCTGCCCTTTCCATGGGAGAGATACTCCCGGCGAGAGCTGGCACCCCTACTTGGAGC 440
QY  544  CACAAGGCGCTGATGTACTGCGCTGCGCTGTACTCTGCTCAGAGGGCGGCCCATGTAGTTGTT 603
DB    441  CACAAGGCGCTGATGTACTGCGCTGCGCTGTACTCTGCTCAGAGGGCGGCCCATGTAGTTGTT 500
QY  604  ACCGCTTCCACTGTCCGCGCTGTCACACTGCCCGCCAGCGCTGTGACGGAGGCCAGCAATGCT 663
DB    501  ACCGCTTCCACTGTCCGCGCTGTCACACTGCCCGCCAGCGCTGTGACGGAGGCCAGCAATGCT 560
QY  664  GTCCCAAGTGTGTGAACCTTCACACTCCCTCTGGACTCCCGGCCCCACCAAGTCTCTGCC 723
DB    561  GTCCCAAGTGTGTGAACCTTCACACTCCCTCTGGACTCCCGGCCCCACCAAGTCTCTGCC 620
QY  724  AGCAACAAGCGGACCATGTACCAACACGGAGAGATCTTCAGTGGCCCATGAGCTGTTCCCTT 783
DB    621  AGCAACAAGCGGACCATGTACCAACACGGAGAGATCTTCAGTGGCCCATGAGCTGTTCCCTT 680
QY  784  CCCGCTGCCCAACAGTGTGTCTCTGAGCTGCAACAGAGGGCCAGATCTACTCGCGCC 843
DB    681  CCCGCTGCCCAACAGTGTGTCTCTGAGCTGCAACAGAGGGCCAGATCTACTCGCGCC 740
QY  844  TCACAACCTGCCCCGAAACAGGCTGCCAGCACCCCTCCCGCTGCCAGACTCTCTGCTGCC 903
DB    741  TCACAACCTGCCCCGAAACAGGCTGCCAGCACCCCTCCCACTGCCAGACTCTCTGCTGCC 800
QY  904  AAGCTGTCAAGATGAGGCAAGTGAACAATCGATGAAGAGGACAGTGTGAGTGCCTGCC 963
DB    801  AAGCTGTCAAGATGAGGCAAGTGAACAATCGATGAAGAGGACAGTGTGAGTGCCTGCC 860
QY  964  ATGGGTGAGACATCTCTCAGGATCCCATGTTTCCAGTGTGCTGGAGAAAGAGAGGCCCGG 1023
DB    861  ATGGGTGAGACATCTCTCAGGATCCCATGTTTCCAGTGTGCTGGAGAAAGAGAGGCCCGG 920
QY  1024  GCACCCGAGCCCCACTTGCGCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC 1083
DB    921  GCACCCGAGCCCCACTTGCGCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC 980
QY  1084  CCAAGGGAGCAGGACGACCAACATGTCAAGATCGTCTGTAAGGAGAAACATAGAAGACCT 1143
DB    981  CCAAGGGAGCAGGACGACCAACATGTCAAGATCGTCTGTAAGGAGAAACATAGAAGACCT 1040
QY  1144  GTGTGCATGGCGGGAAGACGTACTCTCCACGGGAGGTTGGCACCCGGCTTCCTCGCT 1203
DB    1041  GTGTGCATGGCGGGAAGACGTACTCTCCACGGGAGGTTGGCACCCGGCTTCCTCGCT 1100
QY  1204  TCGGCCCTTGGCCCTGCATCTCTATGCACTGTGAGGATGGCGGCCGAGGACTGCGACGCTG 1263

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1101 TGGCCCTTGGCCCTGCATCTCATCTGAGATGCGCCGACGAGTGCACCGGTG 1160
1264 TGACCTTCCACCCAGTACCCCTGCGTCACTCCGAGAGAAAGTGGCTGGAAAGTGTGCA 1323
1161 TGACCTTCCACCCAGTACCCCTGCGTCACTCCGAGAGAAAGTGGCTGGAAAGTGTGCA 1220
1324 AGATTTCACAG 1383
1221 AGATTTCACAG 1280
1384 CCAAGGACCGGGCGGTCTCTGTCACACATCGTATCCCAAGCCAGAGCAACCTGC 1443
1281 CCAAGGACCGGGCGGTCTCTGTCACACATCGTATCCCAAGCCAGAGCAACCTGC 1340
1444 GTCGCTTTGCCCTGGAACACAGAGGCTCGGACTTGGTGAGATCTACCTCTGGAAGCTGG 1503
1341 GTCGCTTTGCCCTGGAACACAGAGGCTCGGACTTGGTGAGATCTACCTCTGGAAGCTGG 1400
1504 TAAAGATGAGAAACTGAGGCTCAGAGAGTGAAGTACCTCGCCCAAGCCACACAGCC 1563
1401 TAAAGATGAGAAACTGAGGCTCAGAGAGTGAAGTACCTCGCCCAAGCCACACAGCC 1460
1564 AGAATCTTCACATTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGGCA 1623
1461 AGAATCTTCACATTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGGCA 1520
1624 CAGCACTTCGAGCTGCTCGCTGGCCGCCACGAAGTCACTGGAACTCTTCTAGCCAG 1683
1521 CAGCACTTCGAGCTGCTCGCTGGCCGCCACGAAGTCACTGGAACTCTTCTAGCCAG 1580
1684 ACCTGAGCTGAAGTCAAGGCTCAGAGAGTGAAGTACCTCGCCCAAGCAATACCAAGACCT 1743
1581 ACCTGAGCTGAAGTCAAGGCTCAGAGAGTGAAGTACCTCGCCCAAGCAATACCAAGACCT 1640
1744 AACAGTTGAGATGAGCTGTAATTTGTTTATTATTAATTAATTAATTAATTAATTAAT 1803
1641 AACAGTTGAGATGAGCTGTAATTTGTTTATTATTAATTAATTAATTAATTAATTAAT 1700
1804 CATAACCATCAAAA 1817
1701 CATTACCTCAAAA 1714

RESULT 8
S-10-199-672-281
Sequence 281, Application US/10199672
Publication No. US2003014842A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: F3430R1C1
CURRENT APPLICATION NUMBER: US/10/199,672
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: US/10/052,586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120

PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 281
LENGTH: 1732
TYPE: DNA
ORGANISM: Homo Sapien
US-10-199-672-281
Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 424 TTGGCTGGAGCCCTCTCGGACTAAATGCGCACTGGTTCGGTTTCCAGGCCCCAGACATGT 483
Db 321 TGGACTCGGCTGTCTGTGTTTCCCTGGACTCCACAGCTCGAGCCGCGCCAGACATGT 380
QY 484 TCTGCTTTTCATGGAAGAGATACCTCCCGGAGAGCTGGCACCCTACTTGGAGC 543
Db 381 TCTGCTTTTCATGGAAGAGATACCTCCCGGAGAGCTGGCACCCTACTTGGAGC 440
QY 544 CACAAGGCTCATGTACTGCTGCGCTGTACTGCTCAGAGGCGCCCATGTGAGTTGTT 603
Db 441 CACAAGGCTCATGTACTGCTGCGCTGTACTGCTCAGAGGCGCCCATGTGAGTTGTT 500
QY 604 ACCGCTCCACTGTCGCGCTGTCCACTGCCCCAGCCTGTGACGAGGCCACAGCAATGCT 663
Db 501 ACCGCTCCACTGTCGCGCTGTCCACTGCCCCAGCCTGTGACGAGGCCACAGCAATGCT 560
QY 664 GTCCAAAGTGTGGAACTCACAATCCTCTGGAATCTCGGAGCTCCGAGGCCACCAAGTCTGCC 723
Db 561 GTCCAAAGTGTGGAACTCACAATCCTCTGGAATCTCGGAGGCCACCAAGTCTGCC 620
QY 724 AGCAACAGGACCATGTATCAACACAGGAGATCTTCACTGCGCCATGAGCTGTTCCCT 783
Db 621 AGCAACAGGACCATGTATCAACACAGGAGATCTTCACTGCGCCATGAGCTGTTCCCT 680
QY 784 CCGCTCTGCCCAACAGTGTCTCTGAGCTGCACAGAGGCCAGATCTACTGCGGCC 843
Db 681 CCGCTCTGCCCAACAGTGTCTCTGAGCTGCACAGAGGCCAGATCTACTGCGGCC 740
QY 844 TCACAACCTGCCCCGAAACAGGCTGCCAGCACCCTCTCCGCTGCCAGACTCTGCTGCC 903
Db 741 TCACAACCTGCCCCGAAACAGGCTGCCAGCACCCTCTCCAGTGCAGACTCTGCTGCC 800
QY 904 AGCTCTCAAGATGAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 963
Db 801 AAGCTCTCAAGATGAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 860
QY 964 ATGGGTGAGACATCTCTCAGGATCCATGTTCCAGTGTGCTGGAGAGAGAGAGGCCCG 1023
Db 861 ATGGGTGAGACATCTCTCAGGATCCATGTTCCAGTGTGCTGGAGAGAGAGAGGCCCG 920
QY 1024 GCACCCAGCCCCCAGCTGGCTCAGGCTCTGAGCTTCACTCCCTCGCCTTCAGAC 1083
Db 921 GCACCCAGCCCCCAGCTGGCTCAGGCTCTGAGCTTCACTCCCTCGCCTTCAGAC 980
QY 1084 CCAAGGAG 1143
Db 981 CCAAGGAG 1040
QY 1144 GTGTGATGCGGGGAG 1203

[illegible]

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RESULT 9
US-10-006-172A-141
; Sequence 141, Application US/10006172A
; Publication No. US20030153000A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Borstein, David
; APPLICANT: Bosnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paori, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmitted
; FILE REFERENCE: P2830P1C11
; CURRENT APPLICATION NUMBER: US/10/006
; PRIORITY FILING DATE: 2002-03-19
; PRIORITY FILING NUMBER: 60/098716
; PRIORITY FILING DATE: 1998-09-01

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; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
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; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
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; PRIOR FILING DATE: 1998-09-30
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; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
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; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
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; PRIOR FILING DATE: 1998-10-08

; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
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; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
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; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 424 TTGGGCTGGAGCTCCTGGGACTAACATGGGACTGGTGGTTTGGCCAGGCCCCAGACATGT 483
DB 321 TGGAGCTGGCGCTGCTGGTTCCCTCCCTGGACTCCACGCTCGAGCCGCGCCAGACATGT 380
QY 484 TCTGCTTTTCCATGGGAAGAGATACTCCCGCGGAGAGCTGGACACCCCTACTTGGAGC 543
DB 381 TCTGCTTTTCCATGGGAAGAGATACTCCCGCGGAGAGCTGGACACCCCTACTTGGAGC 440
QY 544 CACAAGGCTGATGTACTGCTGCTGTACTGCTGTACCTGTCTAGAGGGCGCCCATGTGAGTTGTT 603
DB 441 CACAAGGCTGATGTACTGCTGCTGTACTGCTGTACCTGTCTAGAGGGCGCCCATGTGAGTTGTT 500
QY 604 ACCGCTTCCACTGTCGGCTGTCCACTGCCCCAGGCTGTGAGGAGGCCACAGCAATGCT 663
DB 501 ACCGCTTCCACTGTCGGCTGTCCACTGCCCCAGGCTGTGAGGAGGCCACAGCAATGCT 560
QY 664 GTCCCAAGTGTGGAACTTCCACTGCTGGACTCCCTGAGCTCCGCGGCCCCACCAAGTCTCTGCC 723
DB 561 GTCCCAAGTGTGGAACTTCCACTGCTGGACTCCCTGAGCTCCGCGGCCCCACCAAGTCTCTGCC 620
QY 724 AGCAACACGGGACCATGTACCAACACGAGAGATCTTCACTGCGCCCATGAGCTGTTCCTT 783
DB 621 AGCAACACGGGACCATGTACCAACACGAGAGATCTTCACTGCGCCCATGAGCTGTTCCTT 680
QY 784 CCGGCTTGCCCAACACAGTGTCTCTGAGTGTGACAGTGTGACAGGGCCAGATCTACTCGGGCC 843
DB 681 CCGGCTTGCCCAACACAGTGTCTCTGAGTGTGACAGTGTGACAGGGCCAGATCTACTCGGGCC 740
QY 844 TCACAACCTGCCCCGAAACAGGCTGCCAGCAACCTCCGCTGCCAGACTCCCTGCTGCC 903
DB 741 TCACAACCTGCCCCGAAACAGGCTGCCAGCAACCTCCCTCCACTGCGCAGACTCTCTGCTGCC 800
QY 904 AAGCTTCAAGATGAGGCAAGTGAAGCAATCGATGAGAGGACAGTGTGAGTGTGCTGCC 963
DB 801 AAGCTTCAAGATGAGGCAAGTGAAGCAATCGATGAGAGGACAGTGTGAGTGTGCTGCC 860
QY 964 ATGGGGTGAGACATCTCTCAGGATCAATGTTCCAGTGTGCTGGGAGAAAGAGAGGCCCGG 1023

Db 1221 AGATTGTCAGAGCAAAAGCAGACCCCTGGCCACAGTCAGTCCAGTGTGTC 1280
2Y 1384 CCAAGGCAACCGGCGGGTCTCGTCCACACATCGTATCCCCCAAGCCCAAGACCTGC 1443
Db 1281 CCAAGGCAACCGGCGGGTCTCGTCCACACATCGTATCCCCCAAGCCCAAGACCTGC 1340
2Y 1444 GTCGCTTTGCCCTGGAACACAGAGGCTCGGACTTGGTGGAGATCTACTCTGGAAGCTGG 1503
Db 1341 GTCGCTTTGCCCTGGAACACAGAGGCTCGGACTTGGTGGAGATCTACTCTGGAAGCTGG 1400
2Y 1504 TAAAGATGAGAAACTAGGCTCAGAGAGGTGAAGTACTGCGCCCAAGCCCAACAGCC 1563
Db 1401 TAAAGATGAGAAACTAGGCTCAGAGAGGTGAAGTACTGCGCCCAAGCCCAACAGCC 1460
2Y 1564 AGAATCTTCCACTGACTCAGATCAAGAAAGTCAAGAAAGTCAAGAAAGTCAAGAAAGTCA 1623
Db 1461 AGAATCTTCCACTGACTCAGATCAAGAAAGTCAAGAAAGTCAAGAAAGTCAAGAAAGTCA 1520
QY 1624 CAGCACTTCCGACTGCTCGCTGCGCCCAAGAGGTCACCTGGAAGCTCTTCCCTAGCCAG 1683
Db 1521 CAGCACTTCCGACTGCTCGCTGCGCCCAAGAGGTCACCTGGAAGCTCTTCCCTAGCCAG 1580
QY 1684 ACCCTGGAGCTGAAGGTCAAGGCTCAGAGAGGTGAAGTACTGCGCCCAAGCCCAACAGCC 1743
Db 1581 ACCCTGGAGCTGAAGGTCAAGGCTCAGAGAGGTGAAGTACTGCGCCCAAGCCCAACAGCC 1640
2Y 1744 AACAGTTCAGATATGAGCTGATATTAATTTGTTATTATATTAATTAATTAATTAATTAAT 1803
Db 1641 AACAGTTCAGATATGAGCTGATATTAATTTGTTATTATATTAATTAATTAATTAATTAAT 1700
2Y 1804 CATACCACTCAAAA 1817
Db 1701 CATACCACTCAAAA 1714

RESULT 14
US-10-015-392A-141
; Sequence 141, Application US/10015392A
; Publication No. US20030166901A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C58
; CURRENT APPLICATION NUMBER: US/10/015,392A
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02

; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 141
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-392A-141

Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 424 TTGGGCTGGAGCTCCTCTGGGACTAATCATGTCAGTGGTGGTTTCCAGGCGCCAGACATGT 483
Db 321 TGGGACTCGCGTGTCTGTGTTCCCTTGGACTCCACGCTCGAGCGCGCCAGACATGT 380
QY 484 TCTGCTTTTTCATGGGAAGAGATACTCCCCCGCGGAGAGCTGGCACCCTTACTTTGGAGC 543
Db 381 TCTGCTTTTTCATGGGAAGAGATACTCCCCCGCGGAGAGCTGGCACCCTTACTTTGGAGC 440
QY 544 CACAAGGCTGTAGTACTGCTGCGTGTACTGCTCAGAGGGCGCCCATGTGAGTTGTT 603
Db 441 CACAAGGCTGTAGTACTGCTGCGTGTACTGCTCAGAGGGCGCCCATGTGAGTTGTT 500
QY 604 ACCGCTTCCACTGTCGCGCTTCCACTGCCCCCAGCGCTGTGACGGAGCCACAGCAATGCT 563
Db 501 ACCGCTTCCACTGTCGCGCTTCCACTGCCCCCAGCGCTGTGACGGAGCCACAGCAATGCT 560
QY 664 GTCCCAAGTGTGTGGAACCTCACACTCCCTCTGAGCTCCGCGGCCCCACAAAGTCTCTGCC 723
Db 561 GTCCCAAGTGTGTGGAACCTCACACTCCCTCTGAGCTCCGCGGCCCCACAAAGTCTCTGCC 620
QY 724 AGCAACAACGGGACCATGTATACCAACACGGAGAGATCTTTCAGTGGCCCATGAGCTGTTCCT 783
Db 621 AGCAACAACGGGACCATGTATACCAACACGGAGAGATCTTTCAGTGGCCCATGAGCTGTTCCT 680
QY 784 CCGGCTTCCCAACCAAGTGTCTCTGAGCTGACAGAGGGCCAGATCTACTTGGGCGC 843
Db 681 CCGGCTTCCCAACCAAGTGTCTCTGAGCTGACAGAGGGCCAGATCTACTTGGGCGC 740
QY 844 TCACAACCTGCCCCGAGACAGGCTGCGCCAGCCCTCCGCTGCCAGACTCTCTGCTGCC 903
Db 741 TCACAACCTGCCCCGAGACAGGCTGCGCCAGCCCTCCGCTGCCAGACTCTCTGCTGCC 800
QY 904 AAGCCTGCAAAAGATGAGGCAAGTGAAGATCGGATGAAGAGGACAGTGTGCAAGTCCGCTCC 963
Db 801 AAGCCTGCAAAAGATGAGGCAAGTGAAGATCGGATGAAGAGGACAGTGTGCAAGTCCGCTCC 860
QY 964 ATGGGCTGAGACATCTCTCAGGATCCATGTTTCCAGTGTGTTGGGAGAAAGAGAGCCCGG 1023
Db 861 ATGGGCTGAGACATCTCTCAGGATCCATGTTTCCAGTGTGTTGGGAGAAAGAGAGCCCGG 920
QY 1024 GCACCCGAGCCCGCAGCTGCGCTCAGCGCCCTCTGAGCTTCATCCCTGCGCACTTCAGAC 1083
Db 921 GCACCCGAGCCCGCAGCTGCGCTCAGCGCCCTCTGAGCTTCATCCCTGCGCACTTCAGAC 980
QY 1084 CCAAGGGAGCAGGACAGCAACTGTCAAGATCGTCTGAAGAGGAGAAACATGAAGAGCT 1143
Db 981 CCAAGGGAGCAGGACAGCAACTGTCAAGATCGTCTGAAGAGGAGAAACATGAAGAGCT 1040
QY 1144 GTGTGATGCGCGGAGAGAGCTTCTCCACGCGGAGGTGTGGCACCCTTCCGTGCT 1203
Db 1041 GTGTGATGCGCGGAGAGAGCTTCTCCACGCGGAGGTGTGGCACCCTTCCGTGCT 1100
QY 1204 TCGGCCCCCTTGGCTGATCTCTATGCACTGTGAGGATGCGCCGAGACTGCCAGCGTG 1263
Db 1101 TCGGCCCCCTTGGCTGATCTCTATGCACTGTGAGGATGCGCCGAGACTGCCAGCGTG 1160

RESULT 19
US-10-173-692-281
Sequence 281, Application US/10173692
Publication No. US20030166189A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C20
CURRENT APPLICATION NUMBER: US/10/173,692
CURRENT FILING DATE: 2002-06-17
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 281
LENGTH: 1732
TYPE: DNA
ORGANISM: Homo Sapien
US-10-173-692-281
Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 32; Indels 0; Gaps 0;
Y 424 TTGGGCTGGAGCTCTCTGGGACTAATGAGCACTGGTGGTGGCCAGGCCCCAGACATGT 483
b 321 TGGGACTCGGCTCTCTCTGGTTCCTCCCTGGACTCCAGCTCCAGCCCGCCAGACATGT 380
Y 484 TCTGCTTTTCCATGGGAGAGACTCTCCCGGGAGAGCTGGCACCCTACTTGGAGC 543
b 381 TCTGCTTTTCCATGGGAGAGACTCTCCCGGGAGAGCTGGCACCCTACTTGGAGC 440
Y 544 CACAAGGCTGTACTGCTCGGCTGTACTGCTCAGAGGGCGCCCATGTGAGTTGT 603
b 441 CACAAGGCTGTACTGCTCGGCTGTACTGCTCAGAGGGCGCCCATGTGAGTTGT 500
Y 604 ACCGCTTCCACTGTCCGCTGTCCACTGCCCCAGCTGTGACGGAGCCACAGCAATGCT 563
b 501 ACCGCTTCCACTGTCCGCTGTCCACTGCCCCAGCTGTGACGGAGCCACAGCAATGCT 560
Y 664 GTCCCAAGTGTGGAACTCACACTCCCTCTGGACTCCGGGCCCCACCAAAGTCTGCTCC 723
b 561 GTCCCAAGTGTGGAACTCACACTCCCTCTGGACTCCGGGCCCCACCAAAGTCTGCTCC 620
Y 724 AGCACACGGGACCATGTACCAACAGGAGAGATCTTCAGTGGCCCATGAGCTGTTCCCT 783
b 621 AGCACACGGGACCATGTACCAACAGGAGAGATCTTCAGTGGCCCATGAGCTGTTCCCT 680
Y 784 CCGGCTGCCCCAACAGTGTCTCTCAGTGCACAGAGGGCCAGATCTACTGGGGCC 843
b 681 CCGGCTGCCCCAACAGTGTCTCTCAGTGCACAGAGGGCCAGATCTACTGGGGCC 740
Y 844 TCACAACTGCCCCGAACAGGCTGCCAGCACCCCTCCCGTGGCCAGACTCTCTGTGTC 903
b 741 TCACAACTGCCCCGAACAGGCTGCCAGCACCCCTCCCACTGCGCAGACTCTCTGTGTC 800
Y 904 AAGCTGCAAGATGAGGCAAGTGAAGCAATCGATGAAGAGACAGTGTGCAAGTCTGCTCC 963
b 801 AAGCTGCAAGATGAGGCAAGTGAAGCAATCGATGAAGAGACAGTGTGCAAGTCTGCTCC 860
Y 964 ATGGGGTGAACATCTCTCAGATCCATGTTCCAGTGTGCTGGGAGAAAGAGAGGCCCGG 1023
b 861 ATGGGGTGAACATCTCTCAGATCCATGTTCCAGTGTGCTGGGAGAAAGAGAGGCCCGG 920

QY 1024 GCACCCAGCCCCCACTGGCTCAGCGGCCCTCTGAGCTTCTATCCCTCGCCACTTCAGAC 1083
Db 921 GCACCCAGCCCCCACTGGCTCAGCGGCCCTCTGAGCTTCTATCCCTCGCCACTTCAGAC 980
QY 1084 CCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1143
Db 981 CCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1040
QY 1144 GTGTGCTATGGCGGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1203
Db 1041 GTGTGCTATGGCGGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1100
QY 1204 TCGGCCCCCTTGGCTGCTATCTATGCACTGTGAGGATGGCGCCAGGAGTGCAGAGCTG 1263
Db 1101 TCGGCCCCCTTGGCTGCTATCTATGCACTGTGAGGATGGCGCCAGGAGTGCAGAGCTG 1160
QY 1264 TGACCTGTCCACCGAGTACCTGCTGCTCAGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1323
Db 1161 TGACCTGTCCACCGAGTACCTGCTGCTCAGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1220
QY 1324 AGATTTCGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1383
Db 1221 AGATTTCGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1280
QY 1384 CCAAGGACCCCGGCGGGTCTCTGCTCCACACATCGGTATCCCCAAGCCAGACAACTGC 1443
Db 1281 CCAAGGACCCCGGCGGGTCTCTGCTCCACACATCGGTATCCCCAAGCCAGACAACTGC 1340
QY 1444 GTGCTTTGGCTTGGAAACACAGAGGCTCGGACTTGGTGAGATCTACCTCTGGAAGCTGG 1503
Db 1341 GTGCTTTGGCTTGGAAACACAGAGGCTCGGACTTGGTGAGATCTACCTCTGGAAGCTGG 1400
QY 1504 TAAAGATGAGGAACTGAGGCTCAGAGAGTGAAGTACCTGGCCCAAGGCCACACAGCC 1563
Db 1401 TAAAGATGAGGAACTGAGGCTCAGAGAGTGAAGTACCTGGCCCAAGGCCACACAGCC 1460
QY 1564 AGATCTTCCACTTGGCTCAGATCAAGAAAGTCAAGAAAGTCAAGAAAGTCAAGAAAGGCA 1623
Db 1461 AGATCTTCCACTTGGCTCAGATCAAGAAAGTCAAGAAAGTCAAGAAAGTCAAGAAAGGCA 1520
QY 1624 CAGCACTTCCGACTGCTCGCTGGCCGCCCAAGAGTCACTGGAACCTCTTCTAGCCCCAG 1683
Db 1521 CAGCACTTCCGACTGCTCGCTGGCCGCCCAAGAGTCACTGGAACCTCTTCTAGCCCCAG 1580
QY 1684 ACCCTGAGCTGAAGGTCAAGGCTCAGGAGTCCAGCAAGTGAAGCAAGCAAGCAAGACCT 1743
Db 1581 ACCCTGAGCTGAAGGTCAAGGCTCAGGAGTCCAGCAAGTGAAGCAAGCAAGCAAGACCT 1640
QY 1744 AACAGTTGCAGATATGAGCTGTATTAATTTGTTTATTATATATATATATATATATATAT 1803
Db 1641 AACAGTTGCAGATATGAGCTGTATTAATTTGTTTATTATATATATATATATATATATAT 1700
QY 1804 CATAACCATCAAAA 1817
Db 1701 CATTACCTCAAAA 1714
RESULT 20
US-10-173-694-281
Sequence 281, Application US/10173694
Publication No. US20030166107A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.

APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C19
; CURRENT APPLICATION NUMBER: US/10/173,694
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 281
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-173-694-281

Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 424 TTGGGCTGGAGCCTCTCTGGGACTTAACATGCGACTGTGTCGGTTTCCAGGCGCCAGACATGT 483
DB 321 TGGGACTCGCTGCTGTTTCCCTCGACTCCACGCTCGAGCCCGCCAGACATGT 380
QY 484 TCTGCTTTTCCATGGGAGAGATATCTCCCGCGAGAGCTGSCACCCCTACTTTGGAGC 543
DB 381 TCTGCTTTTCCATGGGAGAGATATCTCCCGCGAGAGCTGSCACCCCTACTTTGGAGC 440
QY 544 CACAAGGCTGATGTACTGCTCGCTGTACTCTGCTCAGAGGCGCCCATGTGAGTTGTT 603
DB 441 CACAAGGCTGATGTACTGCTCGCTGTACTCTGCTCAGAGGCGCCCATGTGAGTTGTT 500
QY 604 ACCGCTCCCACTGTCCGCTGTCCACTGCCGCCAGCCTGTGACGAGGCCACAGCAATGCT 663
DB 501 ACCGCTCCCACTGTCCGCTGTCCACTGCCGCCAGCCTGTGACGAGGCCACAGCAATGCT 560
QY 664 GTCCCAAGTGTGTGGAACCTTCACTCCCTCTGACTCCCGGCCCCCAAGTCTCTGCC 723
DB 561 GTCCCAAGTGTGTGGAACCTTCACTCCCTCTGACTCCCGGCCCCCAAGTCTCTGCC 620
QY 724 AGCACAACGGGACCATGTACCAACAGGAGAGATCTTCACTGAGGAGGCTGTTCCCT 783
DB 621 AGCACAACGGGACCATGTACCAACAGGAGAGATCTTCACTGAGGAGGCTGTTCCCT 680
QY 784 CCGGCTGCCACCACTGCTCTGCTGAGTGCACAGAGGCGCCAGATCTACTGCGGCC 843
DB 681 CCGGCTGCCACCACTGCTCTGCTGAGTGCACAGAGGCGCCAGATCTACTGCGGCC 740
QY 844 TCACAACTTGCCTCCGACCAAGGCTGCCAGCACCCTTCCCTGCCAGCTCTCTGCTGCC 903
DB 741 TCACAACTTGCCTCCGACCAAGGCTGCCAGCACCCTTCCCTGCCAGCTCTCTGCTGCC 800
QY 904 AAGCTTGCAAGATGAGGCAAGTGAAGCAATCGGATGAAGAGACAGTGTGAGTCTGCTCC 963
DB 801 AAGCTTGCAAGATGAGGCAAGTGAAGCAATCGGATGAAGAGACAGTGTGAGTCTGCTCC 860
QY 964 ATGGGTGAGACATCTCAGATCTCATGTTCCAGTGTGCTGGGAGAAAGAGAGGCCCGG 1023
DB 861 ATGGGTGAGACATCTCAGATCTCATGTTCCAGTGTGCTGGGAGAAAGAGAGGCCCGG 920
QY 1024 GCACCCAGCCCTCAGCTGCTGAGCCCTCTGAGCTTCTATCCCTCGCACTTCAGAC 1083
DB 921 GCACCCAGCCCTCAGCTGCTGAGCCCTCTGAGCTTCTATCCCTCGCACTTCAGAC 980
QY 1084 CCAAGGAGAGGAGGAGCAGACAACTGTCAAGATCGTCTGAAGAGAGAAACATAGAAAGCT 1143
DB 981 CCAAGGAGAGGAGGAGCAGACAACTGTCAAGATCGTCTGAAGAGAGAAACATAGAAAGCT 1040
QY 1144 GTGTGATGCGGGAAGAGCTTCTCCACGGGAGGTGTGGCACCCGCTTTCGCTGCT 1203
DB 1041 GTGTGATGCGGGAAGAGCTTCTCCACGGGAGGTGTGGCACCCGCTTTCGCTGCT 1100
QY 1204 TCGGCCCCCTTGCCTGATCTCTATGACCTGTGAGGATGCGCCGCGAGGACTCCAGCGTG 1263
DB 1101 TCGGCCCCCTTGCCTGATCTCTATGACCTGTGAGGATGCGCCGCGAGGACTCCAGCGTG 1160

RESULT 21

US-10-173-698-281
; Sequence 281, Application US/10173698
; Publication No. US20030166108A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C12
; CURRENT APPLICATION NUMBER: US/10/173,698
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 281
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-173-698-281

Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;

Marches	1362;	Conservative	0;	Mismatches	32;	Indels	0;	Gaps	0;
424	TTGGCTGGAGCCTCCTGGGACTAA	CATGGCACTGGTCGGTTTGCAGGCCCCAGACATGT	483						
321	TGGACTCGCGCTGCTCTGGTTCC	CGCTCGCACTCCACGCTCGAGCCGCGCCAGACATGT	380						
484	TCTGCTTTTTCATGGGAAGAGAT	ACTCCCCCGGCGAGAGCTGGCACCCCTACTTGGAGC	543						
381	TCTGCTTTTTCATGGGAAGAGAT	ACTCCCCCGGCGAGAGCTGGCACCCCTACTTGGAGC	440						
544	CACAAGGCTGATGTACTCCCTG	CGCTGTACTCTCAGAGGGCGCCATGTCAAGTTGTT	603						
441	CACAAGGCTGATGTACTCCCTG	CGCTGTACTCTCAGAGGGCGCCATGTCAAGTTGTT	500						
604	ACCGCTCCACTGTCCGCTGTCCA	TGCCCCCAGCCTGTGACGAGCCACACAATGCT	663						
501	ACCGCTCCACTGTCCGCTGTCCA	TGCCCCCAGCCTGTGACGAGCCACACAATGCT	560						
664	GTCCCAAGTGTGGAACTCTACA	CTCATTCCCTCTGGATCTCGGGGCCCAACAAATCTCTGCC	723						
561	GTCCCAAGTGTGGAACTCTACA	CTCATTCCCTCTGGATCTCGGGGCCCAACAAATCTCTGCC	620						
724	AGCAAAAGGGACCATGTATACCA	ACGAGAGATCTTCACTGCTGCGCCATGAGCTTCCCCCT	783						
621	AGCAAAAGGGACCATGTATACCA	ACGAGAGATCTTCACTGCTGCGCCATGAGCTTCCCCCT	680						
784	CCCGCTGCCAACCACTGTCTCT	GTGAGCTGACAGAGGGCCAGATCTACTGGGGCC	843						
681	CCCGCTGCCAACCACTGTCTCT	GTGAGCTGACAGAGGGCCAGATCTACTGGGGCC	740						
844	TCACAACTGCCCCGAAACAGAG	TGCCAGCACCCCTCCGCTGCCAGACTCTCTGTGCC	903						
741	TCACAACTGCCCCGAAACAGAG	TGCCAGCACCCCTCCGCTGCCAGACTCTCTGTGCC	800						
904	AAGCCTGCAAGATGAGGCAAGT	GAGCATCGGATGAAGAGACAGTGTGCATGCTCTCC	963						
801	AAGCCTGCAAGATGAGGCAAGT	GAGCATCGGATGAAGAGACAGTGTGCATGCTCTCC	860						
964	ATGGGTGAGACATCCTCAGGAT	CCATGTTTCAAGTGTCTGGGAGAAAGAGAGGCCCGG	1023						
861	ATGGGTGAGACATCCTCAGGAT	CCATGTTTCAAGTGTCTGGGAGAAAGAGAGGCCCGG	920						
1024	GCACCCAGCCCCCACTGGCCT	CAGCCCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC	1083						
921	GCACCCAGCCCCCACTGGCCT	CAGCCCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC	980						
1084	CCAAGGAGCAGCAGACAACTGT	CAAGATCGTCTGAAGGAGAAACATAAGAAAGCCT	1143						
981	CCAAGGAGCAGCAGACAACTGT	CAAGATCGTCTGAAGGAGAAACATAAGAAAGCCT	1040						
1144	GTGTGATGGCGGGAAGAGCT	ACTCCCAAGGAGGTGGCACCCGCGCTTCCTGTCCT	1203						
1041	GTGTGATGGCGGGAAGAGCT	ACTCCCAAGGAGGTGGCACCCGCGCTTCCTGTCCT	1100						
1204	TGGGCCCTTGCCCTGCACTT	ATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTG	1263						
1101	TGGGCCCTTGCCCTGCACTT	ATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTG	1160						
1264	TGACCTGTCCACCGAGTACCC	TGCCGTCAACCCGAGAAAGTGGCTGGGAAGTGTGCA	1323						
1161	TGACCTGTCCACCGAGTACCC	TGCCGTCAACCCGAGAAAGTGGCTGGGAAGTGTGCA	1220						
1324	AGATTGGCCACAGAGACAAAG	CAGACCTTGGCCACAGTGAGATCAGTTCTACCAAGTGT	1383						
1221	AGATTGGCCACAGAGACAAAG	CAGACCTTGGCCACAGTGAGATCAGTTCTACCAAGTGT	1280						
1384	CCAAGGACACGGGCGGGCTCT	CGTCCACATCGGTATCCCCAAGCCCCAGACAACTGC	1443						
1281	CCAAGGACACGGGCGGGCTCT	CGTCCACATCGGTATCCCCAAGCCCCAGACAACTGC	1340						
1444	GTGCTTTGCCCTGGAAACAG	AGGCTCGGACTTGGTGGAGATCTACCTGTGGAAGCTGG	1503						
1341	GTGCTTTGCCCTGGAAACAG	AGGCTCGGACTTGGTGGAGATCTACCTGTGGAAGCTGG	1400						

```

RESULT 22
US-10-173-698-281
/ Sequence 281, Application US/10173699
/ Publication No. US20030166109A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3430R1C8
/ CURRENT APPLICATION NUMBER: US/10/173,699
/ CURRENT FILING DATE: 2002-06-17
/ Prior Application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 281
/ LENGTH: 1732
/ TYPE: DNA
/ ORGANISM: Homo Sapien
US-10-173-699-281

```

	Query Match	73.9%;	Score 1342.8;	DB 13;	Length 1732;
	Best Local Similarity	97.7%;	0;	Mismatches	32;
	Matches 1362;	Conservative	0;	Indels	0;
	Gaps	0;			
Qy	424	TTGGGCTGGAGCCTCTCGGACTAA	CATGGCACTGGTTCGGTTTCCAGGCCAGACATGT	483	
Db	321	TGGACTCGCGTGTCTGTGTTCC	CCCTGGACTCCACGCTCGAGCCGCGCAGACATGT	380	
Qy	484	TCTCCCTTTTCCATGGGAAGAGATA	CTCCCGCGGAGAGCTGGCACCCCTACTTTGGAGC	543	
Db	381	TCTGCCCTTTCATGGGAAGAGATA	CTCCCGCGGAGAGCTGGCACCCCTACTTTGGAGC	440	
Qy	544	CACAAGGCCTGATGTACTGCCTCG	CGCTGTACCTGCTCAGAGGGCGCCATGTGAGTTGTT	603	
Db	441	CACAAGGCCTGATGTACTGCCTCG	CGCTGTACCTGCTCAGAGGGCGCCATGTGAGTTGTT	500	
Qy	604	ACCGCCTTCACCTGTCCGCGCTGT	CCACTGCCCCCAGCGCTGTGACGGAGCCACAGCAATGCT	663	

Db 501 ACCGCTCCACTGTCCGCTGTCCACTGCCGCCAGCCTGTGACGGAGCCACAGCAATGCT 560
Qy 664 GTCCCAAGTGTGGAACTCACACTCCCTCTGAGCTCCGGGCCCCACCAAGTCTCTGCC 723
Db 561 GTCCCAAGTGTGGAACTCACACTCCCTCTGAGCTCCGGGCCCCACCAAGTCTCTGCC 620
Qy 724 AGCACAACGGGACCATGTATCCAAACGAGAGAGATCTTCAGTGGCCCATGAGCTTCCCT 783
Db 621 AGCACAACGGGACCATGTATCCAAACGAGAGAGATCTTCAGTGGCCCATGAGCTTCCCT 680
Qy 784 CCGGCTGCCCAACCAAGTGTGCTCTGACAGTGCACAGAGGGCCAGATCTACTGGGCC 843
Db 681 CCGGCTGCCCAACCAAGTGTGCTCTGACAGTGCACAGAGGGCCAGATCTACTGGGCC 740
Qy 844 TCACAACCTGCCCGGACCAAGGCTGCCAGCACCCCTCCGCTCCAGACTCTCTGCTGCC 903
Db 741 TCACAACCTGCCCGGACCAAGGCTGCCAGCACCCCTCCGCTCCAGACTCTCTGCTGCC 800
Qy 904 AAGCCTGCAAGATGAGGCAAGTGAAGCAATCGATGAAGAGAGAGTGTGAGTGTCTGCC 963
Db 801 AAGCCTGCAAGATGAGGCAAGTGAAGCAATCGATGAAGAGAGAGTGTGAGTGTCTGCC 860
Qy 964 ATGGGCTGAGACATCTCAGGATCCATGTTTCCAGTGTGAGTGTGAGAGAGAGAGCCGG 1023
Db 861 ATGGGCTGAGACATCTCAGGATCCATGTTTCCAGTGTGAGTGTGAGAGAGAGAGCCGG 920
Qy 1024 GCACCCAGCCCACTGCGCTCAGGCGCCCTCTGAGTTCATCTGCTGCCACTTCAGAC 1083
Db 921 GCACCCAGCCCACTGCGCTCAGGCGCCCTCTGAGTTCATCTGCTGCCACTTCAGAC 980
Qy 1084 CCAAGGAGCAGGACGACACAACTGTCAAGATCGCTGAGGAGAGAGAGAGAGAGGCT 1143
Db 981 CCAAGGAGCAGGACGACACAACTGTCAAGATCGCTGAGGAGAGAGAGAGAGAGGCT 1040
Qy 1144 GTGTGATGCGGGGAGACACTTCTCCACGGGAGGTTGGCACCCGCCCTTCCTGTGCT 1203
Db 1041 GTGTGATGCGGGGAGACACTTCTCCACGGGAGGTTGGCACCCGCCCTTCCTGTGCT 1100
Qy 1204 TCGGCCCCCTTGCCCTGCATCTATGACACTGTGAGGATGGCGCCGAGACTGCCAGGTG 1263
Db 1101 TCGGCCCCCTTGCCCTGCATCTATGACACTGTGAGGATGGCGCCGAGACTGCCAGGTG 1160
Qy 1264 TGACCTGTCCACCGAGTACCCCTGCGCTCACCCGAGAGAGTGGCTGGAGTGTCTGCA 1323
Db 1161 TGACCTGTCCACCGAGTACCCCTGCGCTCACCCGAGAGAGTGGCTGGAGTGTCTGCA 1220
Qy 1324 AGATTTGCCAGAGGACAAAGCAGACCTGCGCCACAGTGAGATCAGTTCTTACAGGTGC 1383
Db 1221 AGATTTGCCAGAGGACAAAGCAGACCTGCGCCACAGTGAGATCAGTTCTTACAGGTGC 1280
Qy 1384 CCAAGGCACCGGGCCGGTCTCTGTCACACATCGGTATCCCCAAAGCCGAGACAACTGC 1443
Db 1281 CCAAGGCACCGGGCCGGTCTCTGTCACACATCGGTATCCCCAAAGCCGAGACAACTGC 1340
Qy 1444 GTCGTTTGCCTTGGAACAGAGGCTCTGGAATTTGGTGGAGATCTACCTCTGGAAGTGG 1503
Db 1341 GTCGTTTGCCTTGGAACAGAGGCTCTGGAATTTGGTGGAGATCTACCTCTGGAAGTGG 1400
Qy 1504 TAAAGATGAGGAACCTGAGGCTCAGAGAGTGAATGCTGGCCCAAGGCCACACAGCC 1563
Db 1401 TAAAGATGAGGAACCTGAGGCTCAGAGAGTGAATGCTGGCCCAAGGCCACACAGCC 1460
Qy 1564 AGAATCTTCACCTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGGCA 1623
Db 1461 AGAATCTTCACCTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGGCA 1520
Qy 1624 CAGCACTTCCGACTGCTGCTGGGCCCCCAGAAAGTCACTGGAAGCTCTTCTAGCCAG 1683
Db 1521 CAGCACTTCCGACTGCTGCTGGGCCCCCAGAAAGTCACTGGAAGCTCTTCTAGCCAG 1580
Qy 1684 ACCCTGAGTGAAGGTGACCGGCTCAGCAAAAGTGAACAAGACATPAAACAAGACT 1743
Db 1581 ACCCTGAGTGAAGGTGACCGGCTCAGCAAAAGTGAACAAGACATPAAACAAGACT 1640

RESULT 23

US-10-173-707-281

; Sequence 281, Application US/10173707

; Publication No. US20030166110A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: F3430R1C17

; CURRENT APPLICATION NUMBER: US/10/173,707

; CURRENT FILING DATE: 2002-06-17

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 281

; LENGTH: 1732

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-173-707-281

Query Match 73.9%; Score 1342.8; DB 13; Length 1732;

Best Local Similarity 97.7%; Pred. No. 0;

Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 424 TTGGGCTGGAGCTCTCTGGGACTAACATGGCACTGGTGGCTTGGCAGGCCCCAGACATGT 483
Db 321 TGGGACTCGCGCTCTCTGGTTCCTCCCTGGACTCCACGCTCGAGCCGCCAGACATGT 380
Qy 484 TCTGCTTTTCCATGGGAAGAGATACCTCCCGCGGAGAGCTGGCACCCCTACTTTGGAGC 543
Db 381 TCTGCTTTTCCATGGGAAGAGATACCTCCCGCGGAGAGCTGGCACCCCTACTTTGGAGC 440
Qy 544 CACAAGGCTGTATGTACTGCTGCTGTACCTGTCTAGAGGGCCGCCATGTGAGTTGTT 603
Db 441 CACAAGGCTGTATGTACTGCTGCTGTACCTGTCTAGAGGGCCGCCATGTGAGTTGTT 500
Qy 604 ACCGCTTCCATGTTCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
Db 501 ACCGCTTCCATGTTCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 560
Qy 664 GTCCCAAGTGTGGAACTCAGACTCCCTCTGAGTCCCGGCCCCACCAAGTCTCTGCC 723
Db 561 GTCCCAAGTGTGGAACTCAGACTCCCTCTGAGTCCCGGCCCCACCAAGTCTCTGCC 620
Qy 724 AGCACAACGGGACCATGTATCCAAACGAGAGAGATCTTCAGTGGCCCATGAGCTGTTCCCT 783
Db 621 AGCACAACGGGACCATGTATCCAAACGAGAGAGATCTTCAGTGGCCCATGAGCTGTTCCCT 680
Qy 784 CCGGCTGCCCAACCAAGTGTCTCTGAGTGCACAGAGGGCCAGATCTTACTGGGCC 843
Db 681 CCGGCTGCCCAACCAAGTGTCTCTGAGTGCACAGAGGGCCAGATCTTACTGGGCC 740
Qy 844 TCACAACCTGCCCGGAAACAGGCTGCCAGCACCCCTCCCGTCCGAGACTCTCTGCTGCC 903

741 TCACAACTGCCCCGAAACGAGCTGCCAGACCCCTCCACTGCCAGACTCTCTGCTGCC 800
904 AAGCCTGCAAGAGTAGGCAAGTAGCAATCGGATGAAGAGACAGTGTGACGTCTGCTCC 963
801 AAGCCTGCAAGAGTAGGCAAGTAGCAATCGGATGAAGAGACAGTGTGACGTCTGCTCC 860
964 ATGGGGTAGACATCCTCAGGATCCATGTTCCAGTATGCTGGAGAAAGAGAGGCCGG 1023
861 ATGGGGTAGACATCCTCAGGATCCATGTTCCAGTATGCTGGAGAAAGAGAGGCCGG 920
1024 GCACCCAGCCCCCACTGGCCTCAGGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC 1083
921 GCACCCAGCCCCCACTGGCCTCAGGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC 980
1084 CCAAGGAGCAGGAGCAGCAACTGTCAAGATCGTCTGAAGAGAAACATTAAGAAAGCCT 1143
981 CCAAGGAGCAGGAGCAGCAACTGTCAAGATCGTCTGAAGAGAAACATTAAGAAAGCCT 1040
1144 GTGTGCATGGCGGAGAGCTACTCTCCACGGGAGGTGTGGCACCGGCCCTCCGTCCT 1203
1041 GTGTGCATGGCGGAGAGCTACTCTCCACGGGAGGTGTGGCACCGGCCCTCCGTCCT 1100
1204 TCGGCCCTTTCCTCTGATCTTATGACCTGTGAGATGGCGCCAGGACTGCCAGCGTG 1263
1101 TCGGCCCTTTCCTCTGATCTTATGACCTGTGAGATGGCGCCAGGACTGCCAGCGTG 1160
1264 TGACCTGTCCACAGTAGTACCTCCCTCCGTCACCCCGAGAAAGTGGTGGAAAGTGTGCA 1323
1161 TGACCTGTCCACAGTAGTACCTCCCTCCGTCACCCCGAGAAAGTGGTGGAAAGTGTGCA 1220
1324 AGATTTGCCAGAGACAAAGCAGACCTCTGGCCACAGTGTGAGATCACTTACCAAGTGTG 1383
1221 AGATTTGCCAGAGACAAAGCAGACCTCTGGCCACAGTGTGAGATCACTTACCAAGTGTG 1280
1384 CCAAGGACACCGGGCGGGTCTCTGTCACACATCGGTATCCCCAAGCCCAAGCAACTGC 1443
1281 CCAAGGACACCGGGCGGGTCTCTGTCACACATCGGTATCCCCAAGCCCAAGCAACTGC 1340
1444 GTCCTTTGCCCTGGAACACAGAGGCTCGGACTGTGAGATCTACCTCTGGAAGCTGG 1503
1341 GTCCTTTGCCCTGGAACACAGAGGCTCGGACTGTGAGATCTACCTCTGGAAGCTGG 1400
1504 TAAAGATGAGAACTGAGGCTCAGAGAGTGAAGTACCTGCGCCCAAGGCCACAGCC 1563
1401 TAAAGATGAGAACTGAGGCTCAGAGAGTGAAGTACCTGCGCCCAAGGCCACAGCC 1460
1564 AGAATCTTCCACTTGACTCAGATCAAGAAAGTCAGGAAGCAAGCTTCCAGAAAGAGGCA 1623
1461 AGAATCTTCCACTTGACTCAGATCAAGAAAGTCAGGAAGCAAGCTTCCAGAAAGAGGCA 1520
1624 CAGCACTTCCGACTGCTCGCTGGCCCCCAGCAAGGTCACTGGAAAGCTTCTTCTAGCCAG 1683
1521 CAGCACTTCCGACTGCTCGCTGGCCCCCAGCAAGGTCACTGGAAAGCTTCTTCTAGCCAG 1580
1684 ACCCTGAGCTGAAGGTCAAGGCTCAGAGAGTCAAGCAAGGTCAAGCAAGCAATTAAGAGCCT 1743
1581 ACCCTGAGCTGAAGGTCAAGGCTCAGAGAGTCAAGCAAGGTCAAGCAAGCAATTAAGAGCCT 1640
1744 AACAGTTGCAGATGAGCTGTATATTTGTTCTTATATATATATATATATATATATATAT 1803
1641 AACAGTTGCAGATGAGCTGTATATTTGTTCTTATATATATATATATATATATATATAT 1700
1804 CATAACCATCAAAA 1817
1701 CATTAACCTCAAAA 1714

RESULT 24
JS-10-174-569-281
; Sequence 281, Application US/10174569
; Publication No. US2003016611A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C39
CURRENT APPLICATION NUMBER: US/10/174,569
CURRENT FILING DATE: 2002-06-18
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 281
LENGTH: 1732
TYPE: DNA
ORGANISM: Homo Sapien
US-10-174-569-281
Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
Qy 424 TTGGGCTGGAGCTCTCTGGGACTAATAGTGGCACTGTGCTGGTTTGGCCAGGCCCGACATGT 483
Db 321 TGGGACTCGCGTGTCTGTGTTTCCCTCGACTCCACGCTCGAGCGCGCCACACATGT 380
Qy 484 TCTGCTTTTCCATGGGAGAGATATCCCGCGGAGAGCTGGCACCCCTACTTTGGAGC 543
Db 381 TCTGCTTTTCCATGGGAGAGATATCCCGCGGAGAGTATCCCGCGGAGAGCTGGCACCCCTACTTTGGAGC 440
Qy 544 CACAAGGCTGATGTACTGCTGCTGCTGTACTGCTCAGAGGGCGCCATGTGAGTTGTT 603
Db 441 CACAAGGCTGATGTACTGCTGCTGCTGTACTGCTCAGAGGGCGCCATGTGAGTTGTT 500
Qy 604 ACCGCTCCACTGTCCGCTGTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
Db 501 ACCGCTCCACTGTCCGCTGTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 560
Qy 664 GTCCCAAGTGTGGAACCTCACACTCTCTGAGTCTGGAGTCTGGGGCCCGCCAAAGTCTGCTGCC 723
Db 561 GTCCCAAGTGTGGAACCTCACACTCTCTGAGTCTGGAGTCTGGGGCCCGCCAAAGTCTGCTGCC 620
Qy 724 AGCAACAGGGAGCCATGTATCCAAACAGGAGATCTTCAAGTCCCATGAGCTGTTCCCTCT 783
Db 621 AGCAACAGGGAGCCATGTATCCAAACAGGAGATCTTCAAGTCCCATGAGCTGTTCCCTCT 680
Qy 784 CCGGCTGCCCAACCCAGTGTCTCTGAGTGTGCAAGAGGGCCAGATCTACTGCGGCC 843
Db 681 CCGGCTGCCCAACCCAGTGTCTCTGAGTGTGCAAGAGGGCCAGATCTACTGCGGCC 740
Qy 844 TCACAACCTGCCCCGAAACAGGCTGCCAGACCCCTCCGCTGCGCCAGATCTCTGCTGCC 903
Db 741 TCACAACCTGCCCCGAAACAGGCTGCCAGACCCCTCCGCTGCGCCAGATCTCTGCTGCC 800
Qy 904 AAGCCTGCAAGAGTAGGCAAGTAGCAATCGATGAAGAGACAGTGTGAGTGTGCTGCC 963
Db 801 AAGCCTGCAAGAGTAGGCAAGTAGCAATCGATGAAGAGACAGTGTGAGTGTGCTGCC 860
Qy 964 ATGGGGTAGACATCCTCAGGATCCATGTTCCAGTATGCTGGAGAAAGAGAGGCCCGG 1023
Db 861 ATGGGGTAGACATCCTCAGGATCCATGTTCCAGTATGCTGGAGAAAGAGAGGCCCGG 920
Qy 1024 GCACCCAGCCCCCACTGGCCTCAGGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC 1083
Db 921 GCACCCAGCCCCCACTGGCCTCAGGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC 980
Qy 1084 CCAAGGAGCAGGAGCAGCAACTGTCAAGATCGTCTGAAGAGAAACATTAAGAAAGCCT 1143


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1221 AGATTGTCCTGAGAGGCAAAAGCAGACCTCTGGCCACAGTGGAGATCAGTTCTTACAGAGTGC 1288
1384 CCAAGGCACGGGCGGGTCTCTCGTCCACACATCGGTATCTCCCAAGCCACAGACAACTGC 1443
1281 CCAAGGCACGGGCGGGTCTCTCGTCCACACATCGGTATCTCCCAAGCCACAGACAACTGC 1340
1444 GTCGCTTTCCCTCTGGAAACACGAGGSCCTCGGACTTGGTGAGATCTTACCTCTGGAAGCTGG 1503
1341 GTCGCTTTCCCTCTGGAAACACGAGGSCCTCGGACTTGGTGAGATCTTACCTCTGGAAGCTGG 1400
1504 TAAAGATGAGGAAACTGAGGCTCAGAGAGTGAAGTACTGTGCCCAAGGCCACAGACC 1563
1401 TAAAGATGAGGAAACTGAGGCTCAGAGAGTGAAGTACTGTGCCCAAGGCCACAGACC 1520
1624 CAGCACTTCGGACTGCTCGCTGSCCCGCCAGAGGTCACCTGGAAACGTCCTTCTAGCCCGAG 1683
1521 CAGCACTTCGGACTGCTCGCTGSCCCGCCAGAGGTCACCTGGAAACGTCCTTCTAGCCCGAG 1580
1684 ACCCTGGAGCTGAAGTCCAGGGCCAGTCCAGACAAAGTGACCAAGACATAAACAAGACCT 1743
1581 ACCCTGGAGCTGAAGTCCAGGGCCAGTCCAGACAAAGTGACCAAGACATAAACAAGACCT 1540
1744 AACAGTTGCAGATATGAGCTGTATAATTGTTTATATATATATATAATAATAAGAGTTG 1803
1641 AACAGTTGCAGATATGAGCTGTATAATTGTTTATATATATATATAATAATAAGAGTTG 1700
1804 CATACCATCAAAA 1817
1701 CATTAACCTCAAAA 1714

RESULT 26
IS-10-174-587-281
Sequence 281, Application US/10174587
Publication No. US20030166113A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P34301C30
CURRENT APPLICATION NUMBER: US/10/174,587
CURRENT FILING DATE: 2002-06-18
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 281
LENGTH: 1732
TYPE: DNA
ORGANISM: Homo Sapien

IS-10-174-587-281

Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred. NO. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

1Y 424 TTGGGCTGGAGCCTCTCGGACTTAACATGSCACTGGTTCGGTTTGCAGGCCCCAGACATGT 483
1B 321 TGGAGCTCGCGTGTCTGTGTTCCCTCGACTCCACCGCTCGAGCGGCCCGCAGACATGT 380
1Y 484 TCTCGCTTTTTCATGGGAAGAGATACTCCCGCGCGAGAGCTGGCACCCCTACTCTGGAGC 543

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381	Db	TTGCTCTTTTCATGGGAAGAGATACTCCCGCGGAGAGCTGGCACCCCTACTTGGAGC	440
544	Qy	CACAGGCGTGATGTACTGCTCGCTGTACTTGTCTCAGAGGGCGCCCATGTGATGTTGTT	603
441	Db	CACAGGCGTGATGTACTGCTCGCTGTACTTGTCTCAGAGGGCGCCCATGTGATGTTGTT	500
604	Qy	ACGCGCTCCACTGTGCGCCTGTGCACCTGCCCCAGCCTGTGACGAGGACACAGCAATGCT	663
501	Db	ACGCGCTCCACTGTGCGCCTGTGCACCTGCCCCAGCCTGTGACGAGGACACAGCAATGCT	560
664	Qy	GTCCCAAGTGTGTGGAACTCCACACTCCCTCTGGACTCCGGGCCCCACCAAAGTCTCTGCC	723
561	Db	GTCCCAAGTGTGTGGAACTCCACACTCCCTCTGGACTCCGGGCCCCACCAAAGTCTCTGCC	620
724	Qy	AGCACACGGGACCATGTACCAACACGGAGAGATCTTCAGTGGCCCATGAGCTGTTTCCCTCT	783
621	Db	AGCACACGGGACCATGTACCAACACGGAGAGATCTTCAGTGGCCCATGAGCTGTTTCCCTCT	680
784	Qy	CCGCGCTGCCCAACCACTGTGTCTCTGACGTGTCACAGAGGGCCAGATCTTACTGCGGCC	843
681	Db	CCGCGCTGCCCAACCACTGTGTCTCTGACGTGTCACAGAGGGCCAGATCTTACTGCGGCC	740
844	Qy	TCACAACTGCCCGGAACCAAGCTGCCAGCACCCCTCCGCTGCCAGACTCTTCTGCTGCC	903
741	Db	TCACAACTGCCCGGAACCAAGCTGCCAGCACCCCTCCGCTGCCAGACTCTTCTGCTGCC	800
904	Qy	AAGCCTGCAAGATGAGCGAAGTGAAGCAATCGGATGAAGAGACAGTGTGCACTCGCTCC	963
801	Db	AAGCCTGCAAGATGAGCGAAGTGAAGCAATCGGATGAAGAGACAGTGTGCACTCGCTCC	860
964	Qy	ATGGGGTGAGACATCTTCAGGATCCATGTTCCAGTGATGCTGGAGAAAGAGAGCCCGG	1023
861	Db	ATGGGGTGAGACATCTTCAGGATCCATGTTCCAGTGATGCTGGAGAAAGAGAGCCCGG	920
1024	Qy	GCACCCAGCCCCCATCTGCGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC	1083
921	Db	GCACCCAGCCCCCATCTGCGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC	980
1084	Qy	CCAAGGAGCAGGACACAACTGTCAAGATCGTTCCTGAGGAGAAACATGAAGAAGCT	1143
981	Db	CCAAGGAGCAGGACACAACTGTCAAGATCGTTCCTGAGGAGAAACATGAAGAAGCT	1040
1144	Qy	GTGTGCATGCGGGAAGACGTACTCCACCGGGAGGTGTGSCACCCGCGCTTCGCTGCT	1203
1041	Db	GTGTGCATGCGGGAAGACGTACTCCACCGGGAGGTGTGSCACCCGCGCTTCGCTGCT	1100
1204	Qy	TCGCGCCCTTTGCCCTGATCCTATGCACTGTGAGGATGGCGCCAGCACTGCCAGCGTG	1263
1101	Db	TCGCGCCCTTTGCCCTGATCCTATGCACTGTGAGGATGGCGCCAGCACTGCCAGCGTG	1160
1264	Qy	TGACCTGTCCACCGAGTACCCCTGCGCTCACCCAGAGAAAGTGGCTGGGAAGTGTCTGCA	1323
1161	Db	TGACCTGTCCACCGAGTACCCCTGCGCTCACCCAGAGAAAGTGGCTGGGAAGTGTCTGCA	1220
1324	Qy	AGATTTGCCACGAGGACAAAGCAGACCCCTGGCCHACAGTGAGATCAGTTCACCAAGTGT	1383
1221	Db	AGATTTGCCACGAGGACAAAGCAGACCCCTGGCCHACAGTGAGATCAGTTCACCAAGTGT	1280
1384	Qy	CCAAGGCACCGGCGCGGTCTCTGTCACATCGGTATCCCCAAGGCCACAGCAACCTGC	1443
1281	Db	CCAAGGCACCGGCGCGGTCTCTGTCACATCGGTATCCCCAAGGCCACAGCAACCTGC	1340
1444	Qy	GTGCTTTGCCCTGGAAACAGAGGCTTCGAGCTTGGTGGAGATCTACTCTTGGAAAGTGG	1503
1341	Db	GTGCTTTGCCCTGGAAACAGAGGCTTCGAGCTTGGTGGAGATCTACTCTTGGAAAGTGG	1400
1504	Qy	TAAAGATGAGGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCCAAGGCCACACAGCC	1563
1401	Db	TAAAGATGAGGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCCAAGGCCACACAGCC	1460
1564	Qy	AGAATCTTCCACTTGACTCAGATCAAGAAAGTCAAGGAAGCAAGACTTCCAGAAAGGCA	1623

1461	AGATCTTCCACTTGATCATCAAGAAAGTCAGGAGCAAGACTTCCAGAAAGAGCA	1520	DB
1624	CAGCACTTCGAGCTGCTGCTGGCCGCCCAAGAGTCACTGGAACGCTTCTTCTAGCCGAG	1683	QY
1521	CAGCACTTCGAGCTGCTGCTGGCCGCCCAAGAGTCACTGGAACGCTTCTTCTAGCCGAG	1580	DB
1684	ACCTGGAGCTGAAGGTCAAGGCTGCGGAGTCCAGACAAAGTGAACAAGACCT	1743	QY
1581	ACCTGGAGCTGAAGGTCAAGGCTGCGGAGTCCAGACAAAGTGAACAAGACCT	1640	DB
1744	AACAGTTCAGATATGAGCTGTATAATTTGTTATTATATATATATAAAGAGTTG	1803	QY
1641	AACAGTTCAGATATGAGCTGTATAATTTGTTATTATATATATAAAGAGTTG	1700	DB
1804	CATAACCATCAAAA	1817	QY
1701	CATTACCTCAAAA	1714	DB
RESULT 27			
US-10-174-589-281			
; Sequence 281, Application US/10174589			
; Publication No. US20030166114A1			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Chen, Jian			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Pan, James			
; APPLICANT: Smith, Victoria			
; APPLICANT: Watanabe, Colin K.			
; APPLICANT: Wood, William I.			
; APPLICANT: Zhang, Zemin			
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
; FILE REFERENCE: ACIDS ENCODING THE SAME			
; FILE REFERENCE: F3430R1C33			
; CURRENT APPLICATION NUMBER: US/10/174,589			
; PRIOR FILING DATE: 2002-06-18			
; Prior Application removed - See File Wrapper or Palm			
; NUMBER OF SEQ ID NOS: 612			
; SEQ ID NO 281			
; LENGTH: 1732			
; TYPE: DNA			
; ORGANISM: Homo Sapien			
US-10-174-589-281			
Query Match 73.9%; Score 1342.8; DB 13; Length 1732;			
Best Local Similarity 97.7%; Pred. No. 0;			
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;			
424	TTGGGCTGGAGCTTCCTGGGACTAACATGCGACATGCGTTCGTTGCGAGGCCGACATGT	483	QY
321	TGGGACTCGCGCTGCTCTGGTTCCCTCCCTGGACTCCACGCTCGAGCCGCGCCAGACATGT	380	DB
484	TCCTGCTTTCCATGGGAAGAGATACCTCCCGGGGAGAGCTGGCACCCCTACTTTGGAGC	543	QY
381	TCCTGCTTTTCCATGGGAAGAGATACCTCCCGGGGAGAGCTGGCACCCCTACTTTGGAGC	440	DB
544	CACAAGCCCTGATGCTGCTGGCTGTACTCTGCTCAGAGGGCGCCCATGTGAGTTGTT	603	QY
441	CACAAGCCCTGATGCTGCTGGCTGTACTCTGCTCAGAGGGCGCCCATGTGAGTTGTT	500	DB
604	ACCGCTTCCACTGTCGCGCTGTCCACTGCCCCCGGAGCTGTGACGGAGCCACAGCAATGCT	663	QY
501	ACCGCTTCCACTGTCGCGCTGTCCACTGCCCCCGGAGCTGTGACGGAGCCACAGCAATGCT	560	DB
664	GTCCCAAGTGTGGAACTTCCACTGCTGAGCTCCGCGGCCGCCCAAGTCTGCTGCC	723	QY
561	GTCCCAAGTGTGGAACTTCCACTGCTGAGCTCCGCGGCCGCCCAAGTCTGCTGCC	620	DB
724	AGCAACAAGGGAGCCATGTACCAACAGCGGAGAGATCTTCAGTGGCCCATGAGCTGTTCCCT	783	QY

Db 1701 CATTACCTCAAAA 1714

RESULT 28
US-10-174-591-281
; Sequence 281, Application US/10174591
; Publication No. US20030166115A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: F3430R1C32
; CURRENT APPLICATION NUMBER: US/10/174,591
; CURRENT FILING DATE: 2002-06-18
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 281
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Homo Sapien
; JS-10-174-591-281

Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

2Y	424	TTGGGTGGAGCTCTCGGACTAATGCACTGGTTCGTTTTCAGGGCCGACATGT	483
2b	321	TGGGACTCGCGTGTCTGTGTTCCCTGACTCCACGCTCGAGCGCGCCAGACATGT	380
2Y	484	TCTGCCTTTTCCATGGGAAGAGATATCCCGCGGAGAGACTGGCACCCCTACTTGGAGC	543
2b	381	TCTGCCTTTTCCATGGGAAGAGATATCCCGCGGAGAGACTGGCACCCCTACTTGGAGC	440
2Y	544	CACAAGCCTGATGTACTGCTCGCTGTACCTGCTCAGAGGGCGCCATGTGAGTTGTT	603
2b	441	CACAAGCCTGATGTACTGCTCGCTGTACCTGCTCAGAGGGCGCCATGTGAGTTGTT	500
2Y	604	ACGCGCTTCCACTGTTCGCGCTGTCCACTGCGCCCGACGCTGTGACGGAGCCACAGCAATGCT	663
2b	501	ACGCGCTTCCACTGTTCGCGCTGTCCACTGCGCCCGACGCTGTGACGGAGCCACAGCAATGCT	560
2Y	664	GTCCCAAGTGTGTGGAACTTCACACTCCCTCTGGACTCCGCGGCGCCACCAAGTCTTGCC	723
2b	561	GTCCCAAGTGTGTGGAACTTCACACTCCCTCTGGACTCCGCGGCGCCACCAAGTCTTGCC	620
2Y	724	AGCAACAACGGGACCATGTATCCAAACAGGAGAGATCTTCAGTGCCCATGAGCTGTTCCTCT	783
2b	621	AGCAACAACGGGACCATGTATCCAAACAGGAGAGATCTTCAGTGCCCATGAGCTGTTCCTCT	680
2Y	784	CCGCGCTGCCAACACAGTGTGTCTCTGACAGTGTGCAAGAGGGCCAGATCTACTCGGGCC	843
2b	681	CCGCGCTGCCAACACAGTGTGTCTCTGACAGTGTGCAAGAGGGCCAGATCTACTCGGGCC	740
2Y	844	TCACACCTTCCCGGACAGGCTGCCAGACCCCTCCGCTGCGCAGACTCTCTGCTGCTGCC	903
2b	741	TCACACCTTCCCGGACAGGCTGCCAGACCCCTCCGCTGCGCAGACTCTCTGCTGCTGCC	800
2Y	904	AAGCCTTGCAAGATGAGGCAAGTGAAGCAATCGGATGAAGAGGACAGTGTGCAGTGCCTCC	963
2b	801	AAGCCTTGCAAGATGAGGCAAGTGAAGCAATCGGATGAAGAGGACAGTGTGCAGTGCCTCC	860
2Y	964	ATGGGGTGAACATCTCTCAGGATCCATGTTTCCAGTGTGCTGGGAGAGAAAGAGAGGCCCGG	1023

APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C59
CURRENT APPLICATION NUMBER: US/10/175,736
CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 281
LENGTH: 1732
TYPE: DNA
ORGANISM: Homo Sapien
US-10-175-736-281

Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 424 TTGGGCTGAGCTCTCTGGGCTAAACATGACACTGGTTCGGTTTCCAGGCCCGACAGATGT 483
DB 321 TGGGACTCGCTGCTCTGGTTCCCTTGGACTCCACGCTCGAGCGCGCCCGACAGATGT 380
QY 484 TCTGCTTTTCCATGGGAGAGATATCTCCCGGCGAGAGCTGGCACCCCTACTTGGAGC 543
DB 381 TCTGCTTTTCCATGGGAGAGATATCTCCCGGCGAGAGCTGGCACCCCTACTTGGAGC 440
QY 544 CACAGGCTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 603
DB 441 CACAGGCTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 500
QY 604 ACCGCTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
DB 501 ACCGCTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 560
QY 664 GTCCCAAGTGTGGAACCTCACTCCCTCTGAGCTCCGGGCGCCCGACCAAGTCTGCTCC 723
DB 561 GTCCCAAGTGTGGAACCTCACTCCCTCTGAGCTCCGGGCGCCCGACCAAGTCTGCTCC 620
QY 724 AGCACAAGCGGACCATGTATCCACACGAGAGATCTTTCAGTCCGCGATGCTGCTCCCT 783
DB 621 AGCACAAGCGGACCATGTATCCACACGAGAGATCTTTCAGTCCGCGATGCTGCTCCCT 680
QY 784 CCGGCTGCGCCCAACCAAGTGTCTCTGAGCTGCACAGAGGCGGCGAGTCTACTGCGGCC 843
DB 681 CCGGCTGCGCCCAACCAAGTGTCTCTGAGCTGCACAGAGGCGGCGAGTCTACTGCGGCC 740
QY 844 TCACAACCTGCGCCGAAACCAAGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 903
DB 741 TCACAACCTGCGCCGAAACCAAGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 800
QY 904 AAGCTTGCAGAGATGAGGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 963
DB 801 AAGCTTGCAGAGATGAGGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 860
QY 964 ATGGGCTGAGACATCTCTGAGATCCATGTTCCAGTGTGCTGGGAGAGAGAGAGAGAGAGAG 1023
DB 861 ATGGGCTGAGACATCTCTGAGATCCATGTTCCAGTGTGCTGGGAGAGAGAGAGAGAGAGAG 920
QY 1024 GCACCCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1083
DB 921 GCACCCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 980
QY 1084 CCAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1143
DB 981 CCAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1040
QY 1144 GTGTGATGCGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1203
DB 1041 GTGTGATGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1100
QY 1204 TCGGCGGCTTGGCTGCTATGATGCTGAGGATGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1263

DB 1101 TCGGCGGCTTGGCTGCTATCTATGCACTGTGAGGATGGCGGCGAGACTGCCAGCGTG 1160
QY 1264 TGACCTGTCCCGAGTACCTGCTGCGGTACCCCGAGAGAAAGTGGCTGGGAGTGTCTGCA 1323
DB 1161 TGACCTGTCCCGAGTACCTGCTGCGGTACCCCGAGAGAAAGTGGCTGGGAGTGTCTGCA 1220
QY 1324 AGATTGGCCGAGAGGACAAAGCAGAGCCCTGGCCACAGTGTGAGTGTCTACAGGTTGTC 1383
DB 1221 AGATTGGCCGAGAGGACAAAGCAGAGCCCTGGCCACAGTGTGAGTGTCTACAGGTTGTC 1280
QY 1384 CCAAGGACCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1443
DB 1281 CCAAGGACCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1340
QY 1444 GTGCTTTGGCTTGGAAACAGAGGCGCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGG 1503
DB 1341 GTGCTTTGGCTTGGAAACAGAGGCGCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGG 1400
QY 1504 TAAAGATGAGGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCC 1563
DB 1401 TAAAGATGAGGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCC 1460
QY 1564 AGAATCTTCCACTGACTCAGATCAAGAAAGTCAAGAGTCAAGAGTCTCCAGAAAGGCA 1623
DB 1461 AGAATCTTCCACTGACTCAGATCAAGAAAGTCAAGAGTCAAGAGTCTCCAGAAAGGCA 1520
QY 1624 CAGCACTTCCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1683
DB 1521 CAGCACTTCCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1580
QY 1684 ACCCTGGAGTGAAGTCAAGGCTCAGGCGGCGGCTCAGAGACAAAGTGAACACATACAAAGACCT 1743
DB 1581 ACCCTGGAGTGAAGTCAAGGCTCAGGCGGCGGCTCAGAGACAAAGTGAACACATACAAAGACCT 1640
QY 1744 AACAGTGTGAGATGAGTGTATTAATTTGTTTATTAATTAATTAATTAATTAATTAATTAATTAAT 1803
DB 1641 AACAGTGTGAGATGAGTGTATTAATTTGTTTATTAATTAATTAATTAATTAATTAATTAATTAAT 1700
QY 1804 CATAACCATCAAAA 1817
DB 1701 CATTACCTCAAAA 1714

RESULT 30
US-10-175-742-281
; Sequence 281, Application US/10175742
; Publication No. US20030166118A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C59
; CURRENT APPLICATION NUMBER: US/10/175,742
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 281
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-742-281

[illegible]

844	2Y	TCAACA	CTGCGCCGCGAACA	CGAGGTGCGCCAGCA	CCCTTCCGCTGCCAGATCTCTGTGTC	903
741	2B	TCAACA	CTGCGCCGCGAACA	CGAGGTGCGCCAGCA	CCCTTCCGCTGCCAGATCTCTGTGTC	800
904	2Y	AAGCCT	GCAAGATGAGGCAAGT	GACCAATCGGATGAAGAGGACAGTGTGCACTGCTGCTCC	963	
801	2B	AAGCCT	GCAAGATGAGGCAAGT	GAGCAATCGGATGAAGAGGACAGTGTGCACTGCTGCTCC	860	
964	2Y	ATGGGG	TGAGACATCTCT	CAGGATCCATGTTTCCAGTGATGCTGGGAGAAAAGAGAGGCCCGG	1023	
861	2B	ATGGGG	TGAGACATCTCT	CAGGATCCATGTTTCCAGTGATGCTGGGAGAAAAGAGAGGCCCGG	920	
1024	2Y	GCACCC	CGCCCGCCACTG	GGCCTCAGCGCCCTCTGAGCTTTCATCCCTCGCCACTTTCAGAC	1083	
921	2B	GCACCC	CGCCCGCCACTG	GGCCTCAGCGCCCTCTGAGCTTTCATCCCTCGCCACTTTCAGAC	980	
1084	2Y	CCNAGG	AGCAGCAGCA	CAACTGTCAAGATCGTCTGAAGAGAAACAATAAGAAAGCCCT	1143	
981	2B	CCNAGG	AGCAGCAGCA	CAACTGTCAAGATCGTCTGAAGAGAAACAATAAGAAAGCCCT	1040	
1144	2Y	GTGTG	CATGCGGGAGAGCGT	ACTCCACGGGAGGTGTGGCACCCGGCCCTTCCTGTCCT	1203	
1041	2B	GTGTG	CATGCGGGAGAGCGT	ACTCCACGGGAGGTGTGGCACCCGGCCCTTCCTGTCCT	1100	
1204	2Y	TGGCC	CCCTTGGCCTGCAT	CTTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTG	1263	
1101	2B	TGGCC	CCCTTGGCCTGCAT	CTTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTG	1160	
1264	2Y	TGACT	TGTCACCGAGTACCC	CTGCGGTCAACCCGAGAAAGTGGTGGGAAGTGTGCA	1323	
1161	2B	TGACT	TGTCACCGAGTACCC	CTGCGGTCAACCCGAGAAAGTGGTGGGAAGTGTGCA	1220	
1324	2Y	AGATTT	GCCCGCAGGACAAAG	CAGACCTGGCCACAGTGAGATCAGTTCTACAGAGTGTC	1383	
1221	2B	AGATTT	GCCCGCAGGACAAAG	CAGACCTGGCCACAGTGAGATCAGTTCTACAGAGTGTC	1280	
1384	2Y	CAAGGC	ACCGGGGCTCTCGT	CCACATCGGTATCCCCAAGCCAGACAACTGC	1443	
1281	2B	CAAGGC	ACCGGGGCTCTCGT	CCACATCGGTATCCCCAAGCCAGACAACTGC	1340	
1444	2Y	GTGCT	TTTGCCCTTGGAAAC	CAGAGGCTTCGACCTTGGTGGAGATCTACTCTGGAAGCTGG	1503	
1341	2B	GTGCT	TTTGCCCTTGGAAAC	CAGAGGCTTCGACCTTGGTGGAGATCTACTCTGGAAGCTGG	1400	
1504	2Y	TAAAGAT	GAGGAACTGAGGCT	CAGAGGTTGAAGTACTGTGCCCAAGGCCACACAGCC	1563	
1401	2B	TAAAGAT	GAGGAACTGAGGCT	CAGAGGTTGAAGTACTGTGCCCAAGGCCACACAGCC	1460	
1564	2Y	AGNAT	CTTCGACTTGACT	CGATCAAGAAAGTCAGGAAGCAAGACTTCCNAGAAGAGGCA	1623	
1461	2B	AGNAT	CTTCGACTTGACT	CGATCAAGAAAGTCAGGAAGCAAGACTTCCNAGAAGAGGCA	1520	
1624	2Y	CAGCA	CTTCGACTGCTCGCT	GGCCCCCAGGAGTCACTGGAAAGCTGCTTCTTAGCCCCAG	1683	
1521	2B	CAGCA	CTTCGACTGCTCGCT	GGCCCCCAGGAGTCACTGGAAAGCTGCTTCTTAGCCCCAG	1580	
1684	2Y	ACCT	GGAGCTGAAGGT	CACGGCCAGTCCAGACAAAGTGACCAAGACATAACAAAGACCT	1743	
1581	2B	ACCT	GGAGCTGAAGGT	CACGGCCAGTCCAGACAAAGTGACCAAGACATAACAAAGACCT	1640	
1744	2Y	AACAGT	TGCAGATATGAGCT	GTATAATTTGTTTATTATATTAATAAAGAGTTG	1803	
1641	2B	AACAGT	TGCAGATATGAGCT	GTATAATTTGTTTATTATATTAATAAAGAGTTG	1700	
1804	2Y	CATAA	CCCTCAAAA	1817		
1701	2B	CATAA	CCCTCAAAA	1714		

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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P34301C62
; CURRENT APPLICATION NUMBER: US/10/175,748
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 281
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-748-281

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RESULT 33
JS-10-175-748-281
; Sequence 281, Application US/10175748
; Publication No. US20030166121A1

1084	QY	CCAAGGAGCAGCAGCAGCAACCTGTGTCAGATCTCTCTGAAGAGAAACATAAGAAAGCCT	1143
981	Db	CCAAGGAGCAGCAGCAGCAACCTGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCT	1040
1144	QY	GTGTGCATGCGCGGAGAGACGTACTCCACGGGAGAGTGTGGCACCCGGCCCTTCCTGTCCT	1203
1041	Db	GTGTGCATGCGCGGAGAGACGTACTCCACGGGAGAGTGTGGCACCCGGCCCTTCCTGTCCT	1100
1204	QY	TCGGCCCCCTTGCCCTGCATCTCATATGCACCTGTGAGGATGSCCGCCAGGACTGCCACGCTG	1263
1101	Db	TGGGCCCCCTTGCCCTGCATCTCATATGCACCTGTGAGGATGSCCGCCAGGACTGCCACGCTG	1160
1264	QY	TGACCTGTGCCACCCGAGTACCCCTGCCGTCAACCCGAGAAAGTGGCTGGGAACTGTGTGCA	1323
1161	Db	TGACCTGTGCCACCCGAGTACCCCTGCCGTCAACCCGAGAAAGTGGCTGGGAACTGTGTGCA	1220
1324	QY	AGATTTTCCACAGGACAAAGCAGACCCCTGGCCACACAGTGCAGATCAGTTCTTACCAGGTGTC	1383
1221	Db	AGATTTTCCACAGGACAAAGCAGACCCCTGGCCACACAGTGCAGATCAGTTCTTACCAGGTGTC	1280
1384	QY	CCAAGCACCGGSCCGGTCCTCGTCCACACATCGGTATCCCCAAGCCACAGACAACTGTC	1443
1281	Db	CCAAGCACCGGSCCGGTCCTCGTCCACACATCGGTATCCCCAAGCCACAGACAACTGTC	1340
1444	QY	GTGCTTTGCCCTTGGAACACAGAGGCTCGGACTTGGTGGAGATCTACTCTGGAAGCTGG	1503
1341	Db	GTGCTTTGCCCTTGGAACACAGAGGCTCGGACTTGGTGGAGATCTACTCTGGAAGCTGG	1400
1504	QY	TAAAGATGAGGAAACTGAGGCTCAGAGAGGTGAGCTACTGTGCGCCACAGCCACACAGCC	1563
1401	Db	TAAAGATGAGGAAACTGAGGCTCAGAGAGGTGAGCTACTGTGCGCCACAGCCACACAGCC	1460
1564	QY	AGAATCTTCACATTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAGAGGCA	1623
1461	Db	AGAATCTTCACATTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAGAGGCA	1520
1624	QY	CAGCACTTCCGACTGTGCTGGCTGGCCCCCAGCAAGGTCACTGGAAACGCTCTTCCTAGCCAG	1683
1521	Db	CAGCACTTCCGACTGTGCTGGCTGGCCCCCAGCAAGGTCACTGGAAACGCTCTTCCTAGCCAG	1580
1684	QY	ACCCCTGGAGCTGAAGGTCAAGGCTGCAAGCAAAAGTGCACCAAGCATAAACAAGACCT	1743
1581	Db	ACCCCTGGAGCTGAAGGTCAAGGCTGCAAGCAAAAGTGCACCAAGCATAAACAAGACCT	1640
1744	QY	AACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATATAATAAATAAGAGTTG	1803
1641	Db	AACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATATAATAAATAAGAGTTG	1700
1804	QY	CATAACCATCAAAA	1817
1701	Db	CATTACCCCTCAAAA	1714

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RESULT 34
US-10-175-751-281
; Sequence 281, Application US/10175751
; Publication No. US20030166122A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zenin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C57
; CURRENT APPLICATION NUMBER: US/10/175.751

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; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 281
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-1751-751-281

Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 424 TTGGGCTCGAGGCTCTCTGGGACTAAATGGCACTGGTTCGGTTTGCAGGCGCCAGACATGT 483
Db 321 TGGGACTCGGCTGTCTGTGTCTCCCTGGACTCCACGCTCGAGCCCGCCAGACATGT 380

QY 484 TCTGCTTTTCCATGGGAAGAGATACTCCCGCGGAGAGCTGGACACCCCTACTTTGGAGC 543
Db 381 TCTGCTTTTCCATGGGAAGAGATACTCCCGCGGAGAGCTGGACACCCCTACTTTGGAGC 440

QY 544 CACAAGGCTGATGTACTGCTTGGCTGTACTCTGTCTCAGAGGGCGCCCATGTGAGTTGTT 603
Db 441 CACAAGGCTGATGTACTGCTTGGCTGTACTCTGTCTCAGAGGGCGCCCATGTGAGTTGTT 500

QY 604 ACCGCTCCACTGTCCGCTGTCCACTGCCGCCAGCCCTGTGACGGAGCCACAGCAATGCT 663
Db 501 ACCGCTCCACTGTCCGCTGTCCACTGCCGCCAGCCCTGTGACGGAGCCACAGCAATGCT 560

QY 664 GTCCCAAGTGTGTGAACCTCACTACCTCTGAGCTCCGCGGCCCCACCAAGTCTCGCC 723
Db 561 GTCCCAAGTGTGTGAACCTCACTACCTCTGAGCTCCGCGGCCCCACCAAGTCTCGCC 620

QY 724 AGCACAACGGGACCATGTATCCAAACGAGAGAGATCTTTCAGTGCCCATGAGCTGTTCCCT 783
Db 621 AGCACAACGGGACCATGTATCCAAACGAGAGATCTTTCAGTGCCCATGAGCTGTTCCCT 680

QY 784 CCGGCTGCCCAACAGTGTCTCTGTGAGTGTGCAAGAGGGCGCAGATCTACTCGGGCC 843
Db 681 CCGGCTGCCCAACAGTGTCTCTGTGAGTGTGCAAGAGGGCGCAGATCTACTCGGGCC 740

QY 844 TCACAACCTGCCCCGAAACGAGCTGCCAGCACCCCTCCGCTGCCAGACTCTCTGCTGCC 903
Db 741 TCACAACCTGCCCCGAAACGAGCTGCCAGCACCCCTCCCACTGCCAGACTCTCTGCTGCC 800

QY 904 AAGCTGCAAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGAGCAAGTGTGCAGTGCTCTCC 963
Db 801 AAGCTGCAAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGAGCAAGTGTGCAGTGCTCTCC 860

QY 964 ATGGGGTGAGACATCTCTAGGATCCATGTTTCAGTGTGATGCTGGGAGAAAGAGAGCCCG 1023
Db 861 ATGGGGTGAGACATCTCTAGGATCCATGTTTCAGTGTGATGCTGGGAGAAAGAGAGCCCG 920

QY 1024 GCACCCGACGCCCTCTGCGCTCAGCGCCCTGTGAGCTTCATCCCTCGCCACTTCAGAC 1083
Db 921 GCACCCGACGCCCTCTGCGCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC 980

QY 1084 CCAAGGGAGCAGGACAGCAAACTGTCAAGTCTGTGAGGATGGCGCCAGCAATGAGAACCT 1143
Db 981 CCAAGGGAGCAGGACAGCAAACTGTCAAGTCTGTGAGGATGGCGCCAGCAATGAGAACCT 1040

QY 1144 GTGTGCAATGGCGGGAGAGCTACTCCACGSGGAGGTGTGSCACCCGCGCTTCCGTCCT 1203
Db 1041 GTGTGCAATGGCGGGAGAGCTACTCCACGSGGAGGTGTGSCACCCGCGCTTCCGTCCT 1100

QY 1204 TCGGCCCTTGGCCCTGCATCTCTATGACCTGTGAGGATGGCGCCAGGACTGCCACGCTG 1263
Db 1101 TCGGCCCTTGGCCCTGCATCTCTATGACCTGTGAGGATGGCGCCAGGACTGCCACGCTG 1160

QY 1264 TGACCTGTCCCAACGAGTACCCCTGCGTCAACCCCGAGAAAGTGGCTGGGAAGTGTGCA 1323
Db 1161 TGACCTGTCCCAACGAGTACCCCTGCGTCAACCCCGAGAAAGTGGCTGGGAAGTGTGCA 1220

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QY	1204	TCGGCCCTTGCCTTGCAATCCTATGCACTGTGAGGATGCCGCCAGGACTGCCACCGTG	1266
DB	1101	TCGGCCCTTGCCTTGCAATCCTATGCACTGTGAGGATGCCGCCAGGACTGCCACCGTG	1160
QY	1264	TGACCTGTCCCACCGAGTACCCTCTGCCGTCACCCCGAGAAGTGGCTGGGAAGTCTCTGCA	1323
DB	1161	TGACCTGTCCCACCGAGTACCCTCTGCCGTCACCCCGAGAAGTGGCTGGGAAGTCTCTGCA	1220
QY	1324	AGATTGCCAGAGACAAAAGCAGACCCCTGGGCCACAGTAGTAGATCAGTTCTTACCAGGTGTC	1383
DB	1221	AGATTGCCAGAGACAAAAGCAGACCCCTGGGCCACAGTAGTAGATCAGTTCTTACCAGGTGTC	1280
QY	1384	CCAAGGCACCGGGCGGGTCCCTCGTCCACACATCGGTATCCCCAAGCCCGACACAACCTGC	1443
DB	1281	CCAAGGCACCGGGCGGGTCCCTCGTCCACACATCGGTATCCCCAAGCCCGACACAACCTGC	1340
QY	1444	GTCCTTTGCCCTGGAACACAGAGGCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGG	1503
DB	1341	GTCCTTTGCCCTGGAACACAGAGGCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGG	1400
QY	1504	TAAAGATGAGAAACTGAGGCTCAGAGAGGTGAAGTACTTGGCCCCAAGGCCACACAGCC	1563
DB	1401	TAAAGATGAGAAACTGAGGCTCAGAGAGGTGAAGTACTTGGCCCCAAGGCCACACAGCC	1460
QY	1564	AGAATCTTCCACTTGACTCAGATCAAGAAGTCAAGNAGCAAGACTTCCAGNAAGAGGCA	1623
DB	1461	AGAATCTTCCACTTGACTCAGATCAAGAAGTCAAGNAGCAAGACTTCCAGNAAGAGGCA	1520
QY	1624	CAGCACITTCGAGTCTGCTGCTGGCCCCCAGGAAGTCACTTGGAAAGTCTTCTAGCCCCAG	1683
DB	1521	CAGCACITTCGAGTCTGCTGCTGGCCCCCAGGAAGTCACTTGGAAAGTCTTCTAGCCCCAG	1580
QY	1684	ACCTTGAGCTGAAGGTCAAGGCTCAGGCGCAGTCCAGACAAAAGTACCAGACATAACAAGACCT	1743
DB	1581	ACCTTGAGCTGAAGGTCAAGGCTCAGGCGCAGTCCAGACAAAAGTACCAGACATAACAAGACCT	1640
QY	1744	AACAGTTGCAGATATGAGCTGTATTAATTGTTGTTTATATATATTAATAAAGAGTTG	1803
DB	1641	AACAGTTGCAGATATGAGCTGTATTAATTGTTGTTTATATATATTAATAAAGAGTTG	1700
QY	1804	CATAACCATCAAAA	1817
DB	1701	CATTACCCCTCAAAA	1714
RESULT 39			
US-10-176-755-281			
; Sequence 281, Application US/10176755			
; Publication No. US20030166127A1			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Chen, Jian			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Pan, James			
; APPLICANT: Smith, Victoria			
; APPLICANT: Watanabe, Colin K.			
; APPLICANT: Wood, William I.			
; APPLICANT: Zhang, Zemin			
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
; FILE REFERENCE: P3430R1C106			
; CURRENT APPLICATION NUMBER: US/10/176,755			
; CURRENT FILING DATE: 2002-06-21			
; Prior Application removed - See File Wrapper or Palm			
; NUMBER OF SEQ ID NOS: 612			
; SEQ ID NO 281			
; LENGTH: 1732			
; TYPE: DNA			
; ORGANISM: Homo Sapien			

Db 441 CACAAGGCGCTGATGTACTGCGCTGTACTGCTCAGAGGGCGCCCAATGTAGTTGTT 500
Qy 604 ACCGCTCTCACTCTGCGCTGTCTCACTGCGCCCGCCAGCTGTGACGGAGCCACAGCAATGCT 663
Db 501 ACCGCTCTCACTCTGCGCTGTCTCACTGCGCCCGCCAGCTGTGACGGAGCCACAGCAATGCT 560
Qy 664 GTCCCAAGTGTGTGAACCTCACATCCCTCTGAGCTCCGGGCCCCCACCACCAAGTCTGCTCC 723
Db 561 GTCCCAAGTGTGTGAACCTCACATCCCTCTGAGCTCCGGGCCCCCACCACCAAGTCTGCTCC 620
Qy 724 AGCACAAGGGGACCATGTATCAACACGGAGAGATCTTCAGTGGCCCATGAGCTGTCCCT 783
Db 621 AGCACAAGGGGACCATGTATCAACACGGAGAGATCTTCAGTGGCCCATGAGCTGTCCCT 680
Qy 784 CCGCCTGCCCCCAACCACTGCTCTGACCTGCACAGAGGGCCAGATCTACTCGGCG 843
Db 681 CCGCCTGCCCCCAACCACTGCTCTGACCTGCACAGAGGGCCAGATCTACTCGGCG 740
Qy 844 TCACAACCTGCCCCGAAACCAAGGCTGCCAGCACCCCTCCCGCTGCCAGACTCTCTGCTGCC 903
Db 741 TCACAACCTGCCCCGAAACCAAGGCTGCCAGCACCCCTCCCACTGCCAGACTCTCTGCTGCC 800
Qy 904 AAGCCTGCAAAAGATGAGCAAGTGAAGCAATCGGATGAAGAGACAGTGTGAGTCTGCTCC 963
Db 801 AAGCCTGCAAAAGATGAGCAAGTGAAGCAATCGGATGAAGAGACAGTGTGAGTCTGCTCC 860
Qy 964 ATGGGTGAGACATCTCTCAGGATCCATGTTCCAGTATGCTGGGAGAAAGAGAGGCCCGG 1023
Db 861 ATGGGTGAGACATCTCTCAGGATCCATGTTCCAGTATGCTGGGAGAAAGAGAGGCCCGG 920
Qy 1024 GCACCCCGAGCCCGACCTGCGCTCAGGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC 1083
Db 921 GCACCCCGAGCCCGACCTGCGCTCAGGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC 980
Qy 1084 CCAAGGAGCAGGAGCAGCACAACTGCTCAAGATGCTCTGAAGAGAGAAACATAGAAAGCCT 1143
Db 981 CCAAGGAGCAGGAGCAGCACAACTGCTCAAGATGCTCTGAAGAGAGAAACATAGAAAGCCT 1040
Qy 1144 GTGTGCATGCGGGAAGACGTACTCCACGGGAGGTGTGGCACCCGGCTTCCTGCTGCT 1203
Db 1041 GTGTGCATGCGGGAAGACGTACTCCACGGGAGGTGTGGCACCCGGCTTCCTGCTGCT 1100
Qy 1204 TCGGCCCCCTTGCCTGTATGTCACCTGTGAGATGGCGCCCGAGACTGCCAGCGTG 1263
Db 1101 TCGGCCCCCTTGCCTGTATGTCACCTGTGAGATGGCGCCCGAGACTGCCAGCGTG 1160
Qy 1264 TGACCTGTCCACAGAGTACCCCTGCGCTCACCCGAGAAAGTGGTGGGAAAGTGTGCA 1323
Db 1161 TGACCTGTCCACAGAGTACCCCTGCGCTCACCCGAGAAAGTGGTGGGAAAGTGTGCA 1220
Qy 1324 AGATTTGCCAGAGGACAAAGCAGACCCCTGGCCACAGTGAGATCAGTTCTACAGGTGTC 1383
Db 1221 AGATTTGCCAGAGGACAAAGCAGACCCCTGGCCACAGTGAGATCAGTTCTACAGGTGTC 1280
Qy 1384 CCAAGGACCCGGGCGGGTCTCTGTCACATCGGTATCCCAAGCCCGAGCAACCTGC 1443
Db 1281 CCAAGGACCCGGGCGGGTCTCTGTCACATCGGTATCCCAAGCCCGAGCAACCTGC 1340
Qy 1444 GTGCTTTGCCCTGGAAACAGAGGCTCGGACTTGGTGAGATCTACCTTGGAAAGTGG 1503
Db 1341 GTGCTTTGCCCTGGAAACAGAGGCTCGGACTTGGTGAGATCTACCTTGGAAAGTGG 1400
Qy 1504 TAAAGATGAGGAAACTGAGGCTCAGAGAGTGAAGTACTGGCCCAAGGCCACACAGCC 1563
Db 1401 TAAAGATGAGGAAACTGAGGCTCAGAGAGTGAAGTACTGGCCCAAGGCCACACAGCC 1460
Qy 1564 AGAATCTTCCACTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCA 1623
Db 1461 AGAATCTTCCACTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCA 1520
Qy 1624 CAGCACTTCCGACTGCTGCTGGCCCCCAGAGGTCACTGGAAAGTCTTCTTAGGCCAG 1683
Db 1521 CAGCACTTCCGACTGCTGCTGGCCCCCAGAGGTCACTGGAAAGTCTTCTTAGGCCAG 1580

Qy 1684 ACCCTGGAGCTGAAGTCAAGGCTCAGGCGCAGTCCAGACAAAGTGACCAAGACATACAAAGACCT 1743
Db 1581 ACCCTGGAGCTGAAGTCAAGGCTCAGGCGCAGTCCAGACAAAGTGACCAAGACATACAAAGACCT 1640
Qy 1744 AACAGTTGCAGATATGAGCTGTATTAATTGTTTATTATATTAATAATAAAGAGTTG 1803
Db 1641 AACAGTTGCAGATATGAGCTGTATTAATTGTTTATTATATTAATAATAAAGAGTTG 1700
Qy 1804 CATAACCATCAAAA 1817
Db 1701 CATTACCTCAAAA 1714

Search completed: January 31, 2004, 06:00:50
Job time : 656 secs